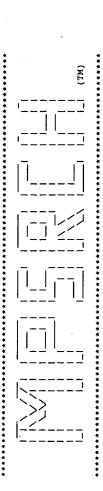
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (C) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Wed Jun 16 13:13:53 1999; MasPar time 3.60 Seconds 100.489 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-027-777B-1 (1-17) from USO9027777B.pep 137 1 CFGGRMDRIGAQSGLGC 17 Title:

Description: Perfect Score:

PAM 150 Gap 15 Scoring table: Seguence:

170751 segs, 21266608 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

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Mean 19.929; Variance 62.491; scale 0.319 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ					
Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description	Pred. No.
	137	100.0	19	-	P80902	Ruman cardiodilatin f	5.630-08
7	137	100.0	20	~	R04085	Sequence encoded by h	5.63e-08
٣	137	100.0	20	7	R40480	[D-Cys146]hANVP(127-1	5.63e-08
4	137	100.0	21	7	R40641	[Arg129][D-Cys146]hAN	5.63e-08
S	137	100.0	21.	7	R40647	[Arg129][D-Ser148]hAN	5.63e-08
9	137	100.0	22	35	W70089	Alpha human atrial na	5.63e-08
7	137	100.0	22	H	P82832	Human Atrial Natriure	5.63e-08
80	137	100.0	22	7	R40646	[Arq129][D-Ser148]hAN	5.63e-08
6	137	100.0	23	7	R40651	[D-Arg129]hANVP(130-1	5.63e-08
10	137	100.0	23	7	R40645	[Arq129][D-Ser148]han	5.63e-08
11	.137	100.0	23	7	R40395	hANVP(127-149)-NH2.	5.63e-08
12	137	100.0	25	~	P71467	Sequence of aldostero	5.63e-08
13	137	100.0	25	7	R40509	[D-Ser128]rANVP(126-1	5.63e-08
14	137	100.0	25	7	R40482	[D-Asn147]rANVP(127-1	5.63e-08
15	137	100.0	25	7	R40475	[D-Cys146]hANVP(127-1	5.63e-08
16	137	100.0	25	7	R40494	[D-Phe149]hANVP(127-1	5.63e-08

19 AA;

Sequence.

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1139]rANVP(126 1148]rANVP(127 126]hANVP(127 126]hANVP(127 126]hANVP(127 126]hANVP(127 126]hANVP(127 126]hANVP(127 127 127 127 127 127 127 127 127 127	tri tri tri tri tri tri tri tri tri ard
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ALIGNMENTS

RESULT 1 ID D80902 standard: protein: 19 aa		_	_	Homo sapiens.	FT disulfide_bond 218	n)	FT /label-OTHER	FT /note="Further peptide fragment of ANF/CDD 1-126	FT misc_difference 19	FT /label-OTHER	FT /note="As above"	PN W08806596-A.	PD 07-SEP-1988.	PF 27-FEB-1988; E00144.	PR 09-DEC-1987; DE-741641,	PI Forssmann WG, Becker G, Herbst F;	DR WPI; 88-271140/38.		PS Claim 1; Page 24; 42pp; German.	CC It has the AA sequence 95-126 of ANF/CDD 1-126 (gamma-hANaP). It may be	CC isolated from human urine by adsorption with alginic acid. It may also be	CC synthesised or prepd. by fragment synthesis, e.g. using ANF/CDD 99-126	CC and the tetrapeptide Thr-Ala-Pro-Arg. It can be used in differentiated	CC vasodilation diagnostics and therapy of hypertonia, application as a	CC substn. for patients which have been implanted with artificial hearts &	CC synchronous regulation of blood volume and electrolytes of the blood. It		CC differential diagnostics of endothelial changes.

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Location/Qualifiers disulfide_bond 2..18 misc_difference 18
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R40647 standard; Protein; 21 AA.
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R40641 standard: Protein; 21 AA.
R40641;
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Best Local Similarity 100.0%;
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Matches 17; Conservative
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01-JUN-1984; US-616488.
08-MAY-1985; US-766030.
05-JUN-1986; US-870795.
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WPI; 93-175525/21
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mlsc_difference
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09-APR-1984;
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Probes were derived by assuming conservation between human atrial
and porcine brain natriuretic peptide, and used to isolate the pBNP gene.
See also 002845.
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14.5EP-1993 (first entry)
16.Cys146]haNVP(127-146)-NH2.
Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
regulation; fluid volume; blood pressure.
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                                                                                                                                                                                                                                                                 01-JUN-1990 (first entry)
Sequence encoded by human natriuretic peptide cDNA.
Porcine BNP: natriuretic; diuretic; vasodilator; hypertension.
Sus scrofa.
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Pred. No. 5.63e-08;
....matches 0; Indels
  Score 137; DB 1; Length 19; Pred. No. 5.63e-08;
                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New natriuretic and vasodilator peptides - obtd. using encoding porcine brain natriuretic peptide and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-DEC-1989.
31-MAY-1989; 02373.
31-MAY-1988; US-2006470.
14-UNW-1988; US-299880.
(CALB) Callf Blotech Inc.
Sellhamer JJ, Lewicki J, Scarborough RM, Porter GJ; WPI; 90-007453/01.
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20
/note= "Amidated C-terminal"
                                                        0; Mismatches
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R40480 standard; Protein; 20 AA.
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R04085 standard; protein; 20 AA
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01-JUN-1984; US-616488.
08-MAY-1985; US-766030.
05-JUN-1986; US-870795.
(SCIO-) SCIOS NOVA INC.
LEWICKI JA. SCARBOROUGH RM;
WPI: 93-175525/21.
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Best Local Similarity 100.0%;
Matches 17; Conservative
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09-APR-1984; 602117
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Disclosure: Column 49: 45pp; English.
The sequences given in R40387-748 are atrial natriuretic/
vasodilator peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of fillid volume and blood pressure in host organisms.
These ANVP fragments may be produced by solid-phase techniques. See also R36937-78.
for regulation of fluid volume and blood pressure in host organisms. These ANVP fragments may be produced by solid-phase techniques. See also R36937-78.
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R40647;
[4.5EP-1993 (first entry)
[4.5Ep-1993 (first entry)
[4.5Ep-1993 (first entry)
[4.5Ep-1993 entry entry entry entry entry)
regulation; fluid volume; blood pressure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-SEP-1993 (first entry)
[Arg12][D-78146]hANVP(129-149)-NH2.
Human; pre-pro: atrial natriuretto/vasodilator peptide; ANVP;
regulation; fluid volume; blood pressure.
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Pred. No. 5.63e-08;
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Pred. No. 5.63e-08;
0; Mismatches 0;
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Human Atrial Natriuretic Polypeptide analogue - having strong diuretic,
   Human Atrial Natriuretic Polypeptide analogue.
Human atrial natriuretic polypeptide; hypotensive; diuretic; beta-LANP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Column 49; 45pp; English.
The sequences given in R40387-748 are atrial natriuretic/
vasodilator peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of fluid volume and blood pressure in host organisms.
These ANVP fragments may be produced by solid-phase techniques. See also R36937-78.
                                                                                                                                                                                 natriuretic and hypotensive action.

Claim 1; page 2; 20pp; English.

This sequence differs from that of natural human atrial natriuretic polypeptide (hAMP) in that the N-terminal 6 residues are deleted. It is present in dimeric form and is useful as a diuretic, natriuretic or hypotensive. It has an application in the treatment or prevention of e.g. cardiac cedema or malignant hypertension.

It is an intermediate for the synthesis of beta-LAMP or analogues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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regulation; fluid volume; blood pressure.
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                                                                                                                                                                                                                                                                                                                                                     Score 137; DB 1; Length 22;
Pred. No. 5.63e-08;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 137; DB 7; Length 22;
Pred. No. 5.63e-08;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-SEP-1993 (first entry)
[Arg129][D-Ser148]hANVP(130-150)-NH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        location/Qualifiers disulfide_bond 2..18 misc_difference 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       л 8
R40646 standard; Protein; 22 AA.
                                                    EP-20000
04-MAY-1988.
26-OCT-1987; 202052.
27-OCT-1986; JP-255312.
(SHIO) Shiomogi Selyaku KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lewicki JA, Scarborough RM;
WPI; 93-175525/21.
                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.0%;
les 17; Conservation
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Local Similarity 100.0%;
les 17; Conservative
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09-APR-1984; 602117.
09-APR-1984; US-602117.
01-JUN-1984; US-616488.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-MAY-1985; US-766030
05-JUN-1986; US-870795
(SCIO-) SCIOS NOVA INC.
Lewicki JA, Scarboroug
                                                                                                                                   Kambayashi Y, Inou
WPI; 88-121118/18.
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Matches
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This represents a human alpha atrial natriuretic peptide sequence (alpha-hANP). The invention provides a composition for treating cardiac diseases associated with cardiac hypertrophy. The composition comprises an active ingredient capable of binding to the peptide receptor of GC-A and promoting production of cGMP. The drug composition may be used cilically to treat cardiac diseases caused by cardiac hypertrophy, including chronic heart failure, ischeamer cardiac diseases and arrhythmia. The active substance can bind to the natriuretic peptide receptor of GC-A and promote production of cGMP, effectively preventing cardiac hypertrophy and leading to improvement of the pulmonary blood circulation. The substance does not affect haemodynamic properties, blood pressure, heart beat and urine volume.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-OCT-1998 (first entry)
Alpha human atrial natriuretic peptide (alpha-hANP) 2 (residues 7-28).
ANP: atrial natriuretic peptide: cardiac disease; cardiac hypertrophy; chronic heart failure; ischaemic cardiac disease; arrhythmia; cGMP; pulmonary blood circulation; haemodynamic property.
                                                                                                                                                       Disclosure: Column 9: 45pp; English.

The sequences given in 840387-748 are atrial natriuretic/
vascollator peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of fluid volume and blood pressure in host organisms.

These ANVP fragments may be produced by solid-phase techniques. See also R36937-78.
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                                                                                                                                New polypeptide cpd. - useful as natriuretic, diuretic and/or
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Pred. No. 5.63e-08;
0; Mismatches 0;
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Pred. No. 5.63e-08;
                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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05-FEB-1997; JP-022594.
CSUNR) SUNTORY LTD.
FUTUYR M, HIGARA T, INOMATA N, YAMAKI A;
WPI; 98-446949/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Examples; Page 23; 35pp; Japanese.
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W70089 standard; peptide; 22 AA.
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                                                                                               Lewicki JA, Scarborough RM; WPI; 93-175525/21.
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Best Local Similarity 100.0%;
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Best Local Similarity 100.0%;
Matches 17; Conservative
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04-DEC-1990 (first entry)
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             09-APR-1984; US-602117.
01-JUN-1984; US-616488.
08-MAY-1985; US-766030.
05-JUN-1986; US-870795.
                                                                                                                                                   vasodilator in mammals
                                                                              (SCIO-) SCIOS NOVA INC
Lewicki JA, Scarborou
                                                                                                                                                                                                                                                                    21 AA;
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Query Match
Best Local Similarity 100.0%;
Matches 17; Conservative
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09-APR-1984; US-602117.
00-JUN-1984; US-61648E.
08-MAY-1985; US-61648E.
05-JUN-1986; US-870795.
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Lewicki JA, Scarborou
WPI; 93-175525/21.
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17-AUG-1984; 642131
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modified_site
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Disclosure; Column 49; 45pp; English.
The sequences given in R0387-748 are atrial natriuretic/
vasodilator peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of fluid volume and blood pressure in host organisms.
These ANVP fragments may be produced by solid-phase techniques. See also R36937-78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vasodilator in mammals
Disclosure: Column 49: 45pp; English.
The sequences given in R40387-748 are atrial natriuretic/
vasodilator peptide (ANVP) cDNAs. These ANVP fragments may be used
for regulation of fluid volume and blood pressure in host organisms.
These ANVP fragments may be produced by solid-phase techniques. See
also R36937-78
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R40645 standard; Protein; 23 AA.
R40645;
14-SEP-1993 (first entry)
Arg1299][D-SeridalhANVP(130-151).
Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
regulation; fluid volume; blood pressure.
                                                                                                  14-SEP-1993 (first entry)
[D-Arg129]hANVP(i30-151).
[Imman: pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat; regulation; fluid volume; blood pressure.
Synthetic.
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WPI; 93-175525/21
New polypeptide cpd. - useful as natriuretic, diuretic and/or
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Pred. No. 5.63e-08;
0; Mismatches 0; Indels
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                                        R40651 standard; Protein; 23 AA. R40651;
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Lewicki JA, Scarborough RM;
WPI; 93-175525/21.
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Best Local Similarity 100.0%;
Matches 17; Conservative
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09-APR-1984; 602117.
09-APR-1984; US-602117.
01-JUN-1984; US-6126488.
08-MAY-1985; US-766030.
05-JUN-1986; US-766030.
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18-MAY-1993.

09-APR-1984; 602117.

09-APR-1984; US-602117.

01-JUN-1984; US-616488.

01-JUN-1984; US-616488.

05-JUN-1986; US-766030.

05-JUN-1986; US-766030.

(SCIO-) SCIOS NOVA INC.
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misc_difference
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                                                     Gaps
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(SALK ) SALK INST FOR BIOL STUD. .
Baird J. Barch 1987.09.
WPI: 87-064498/09.
Aldosterone inhibiting polypeptide - for controlling aldosterone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P71467 standard; peptide; 25 AA.
P71467;
25-APR-1991 (first entry)
Sequence of aldosterone inhibiting polypeptide,
[desArg32]-hAPR(8-33).
Aldosterone dependent hypertension; atrial peptide; natruretic;
diuretic; smooth muscle relaxant.
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Score 137; DB 7; Length 23;
Pred. No. 5.63e-08;
...ant-rhes 0; Indels
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Pred. No. 5.63e-08;
0; Mismatches 0; Indels
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5..21
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Best Local Similarity 100.0%;
Matches 17; Conservative
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Gaps

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Score 137; DB 7; Length 23, Pred. No. 5.63e-08; ''...marches 0; Indels

Wed Jun 16

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Disclosure; Column 36; 45pp; English.
The sequences given in R40387-748 are atrial natriuretic/
vasodilator peptide (ANVP) cDNAs. These ANVP fragments may be used
for regulation of fluid volume and blood pressure in host organisms.
These ANVP fragments may be produced by solid-phase techniques. See
also R36937-78.
09-APR-1984; US-602117.
01-UNN-1984; US-616488.
08-MAY-1985; US-616488.
08-MAY-1985; US-6030.
05-UNN-1986; US-870795.
(SCIO-) SCIOS NOVA INC.
Lewicki JA, Scarborough RM;
WPI: 93-175525/21.
New polypeptide cpd - useful as natriuretic, diuretic and/or
                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                17; Conservative
                                                                                                               vasodilator in mammals
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                                                                                                                                                                                                            25 AA;
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09-APR-1984;
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The sequences given in R40387-748 are atrial natriuretic/
vasodilator peptide (ANVP) cDNAs. These ANVP fragments may be used
for regulation of fluid volume and blood pressure in host organisms.
These ANVP fragments may be produced by solid-phase techniques. See
also R36937-78.
                                                                                                                                        Gaps
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Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
regulation; fluid volume; blood pressure.
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regulation; fluid volume; blood pressure.
                          Aldosterone secretion is inhibited by the administration of a peptide of the invention and its addition salt. It is used for treatment of aldosterone dependent hypertension. Atrial peptides have matruretic, diuretic and smooth muscle relaxant activities. Sequence 25 AA;
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Pred. No. 5.63e-08;
0; Mismatches 0; Indels
                                                                                                           Score 137; DB 2; Length 25;
Pred. No. 5.63e-08;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                    /note= "D-form residue"
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                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                  14pp; English
                                                                                                                                                                                                                                    .T 13
R40509 standard; Protein; 25 AA.
R40509;
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Lewicki JA, Scarborough RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.0%;
Matches 17: Conservation
                                                                                                         Query Match
Best Local Similarity 100.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R40482;
14-SEP-1993 (first entry)
[D-Asn147]rANVP(127-151).
                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                5 cfggrmdrigaqsglgc 21
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09-APR-1984; US-602117.
01-JUN-1984; US-616488.
08-MAY-1985; US-766030.
05-JUN-1986; US-870795.
 dependent hypertension
Example; column 11; 14;
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09-APR-1984; 602117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 AA;
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misc_difference
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The sequences given in R40387-748 are atrial natriuretic/vasodilator peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of fluid volume and blood pressure in host organisms. These ANVP fragments may be produced by solid-phase techniques. See also R36937-78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                  14-SEP-1993 (first entry)
[D-Cys146]hANVP(127-151).
Human: pre-pro: atrial natriuretic/vasodilator peptide; ANVP; rat; regulation; fluid volume; blood pressure.
Synthetic.
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Pred. No. 5.63e-08;
0; Mismatches 0;
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                                                                                                                    T 15
R40475 standard; Protein; 25
R40475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scarborough RM;
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Best Local Similarity 100.0%;
                           1 CFGGRMDRIGAQSGLGC 17
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4 cfggrmdrigagsglgc 20
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01-JUN-1984; US-616488.
08-MAY-1985; US-766030.
05-JUN-1986; US-870795.
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Lewicki JA, Scarborou
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Release 3.1A . Copyright (c)	**************************************	**************************************	**
MPsrch_pp protein - p	protein database search,	th, using Smith-Waterman algorithm	mrl.
Run on: Wed Jun	ın 16 13:16:47 1999;	MasPar time 1.42 Seconds	
Tabular output not gene	generated.	o million cell	
Title: >US-09 Description: (1-17) Perfect Score: 137 Sequence: 1 CFGGI	-027-777B-1 from USO9027777B.pe RMDRIGAQSGLGC 17	a.	
Scoring table: PAM 15 Gap 15	09		
Searched: 106580) segs, 10152877 residues	lues .	-
Post-processing: Minimum Listing	um Match 0% ng first 45 summaries		
Database: a-issued 1:5A_C(led A_COMB 2:5B_COMB 3:PCT9_	F9_COMB 4:backfiles1	
Statistics: Mean 1	18.618; Variance 55.	964; scale 0.333	-
Pred. No. is the nu score greater than and is derived by a	number of results an or equal to the ganalysis of the	predicted by chance to have a score of the result being printed total score distribution.	
d	SUMMARIES		
Result Query No. Score Match Le	Length DB ID	Description Pred. No	
1 137 100.0 2 137 100.0 4 137 100.0 6 137 100.0 7 137 100.0 8 137 100.0 13 137 100.0 10 137 100.0 11 137 100.0 13 137 100.0 14 137 100.0 15 137 100.0 16 137 100.0 17 137 100.0 18 137 100.0 19 137 100.0 20 137 100.0 21 137 100.0 22 137 100.0	17 2 US-08-737- 20 4 5212286-30 23 4 5212286-40 23 4 5212286-50 23 1 US-07-828- 25 4 5212286-28 25 4 5212286-28 25 4 5212286-27 27 4 520239-16 27 4 520239-16 28 4 546142-1 28 4 546142-1 28 1 US-07-781- 28 1 US-07-781-	Sequence 1, Applicatio 4 72e-09 Patent No. 5312286. 4 72e-09 Patent No. 520239. 4 72e-09 Patent No. 520437. 4 72e-09 Patent No. 5404142. 4 72e-09 Patent No. 5404142. 4 72e-09 Patent No. 5404142. 4 72e-09 Sequence 1, Applicatio 4 72e-09	, aaaaaaaaaaaaaaa

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Sequence 1, Application US/08737927

Sequence 1, Soforas

Date: No. 576723

CENERAL INFORMATION:

APPLICANT: IMMER, Hansueli

APPLICANT: FORSAMAN, Wolf-Georg

APPLICANT: ADERMANN, Wolf-Georg

APPLICANT: ALESSEN, Christian

TITLE OF INVENTION: PREPARING CARDIODILATIN FRAGMENTS, AND HIGHLY PURIF

TITLE OF INVENTION: CARDIODILATIN FRAGMENTS, AND HIGHLY PURIF

TITLE OF INVENTION: CARDIODILATIN FRAGMENTS, AND HIGHLY PURIF

TITLE OF INVENTION: ADDRESS:

ADDRESSEE: Nikaido, Marmelstein, Murray & Oram

STREET: 655 Fifteenth Street N.W. Suite 330

CITY: Washington

STRIE: D.C.

COUNTY: Washington

STRIE: D.C.

COMPUTER READABLE FORM:

MEDIUM TYPE: Flopy disk

COMPUTER PROBABLE FORM:
                               726-09
7726-09
7726-09
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7726-09
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7726-09
                            Sequence 3, Application Sequence 2, Application Sequence 18, Application Patent No. 5202239.
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APPLICATION NUMBER: US/08/737,927 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 5
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: W0 95/33769
FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kitts, Monica C.
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P1614-605
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-5000
ITELEPHONE: (202)638-4810
INFORMATION FOR SEQ ID NO: 1:
US-08-470-
US-08-184-
US-08-451-
US-08-284-
US-07-754-
US-08-284-
US-08-48-
S449751-1
5449751-1
5449751-1
542731-1
US-08-48-
US-08-737-
US-08-737-
US-08-737-
US-08-451-
US-08-4
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PEPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
PEPTIDE COMPUNDS
NUMBER OF SEQUENCES: 68
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/870,795
FILING DATE: 05-JUN-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 766,030
FILING DATE: 08-MAY-1985
APPLICATION NUMBER: 602,117
                                                                                                                                                            Score 137; DB 4; Length 22; Pred. No. 4.72e-09;
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APPLICANT: LEWICKI, JOHN A.: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
PEPTIDE COMPUNDS
NUMBER OF SEQUENCES: 68
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/07/870,795
FILING DATE: 05-JUN-1986
PRIOR APPLICATION DATA:
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4.72e-09;
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Pred. No. 4.
                                                                        SEQ ID NO:40:
LENGTH: 22
LENGTH: 24 AA; 2609 MW; 2891 CN;
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ICE 25 AA; 2627 MW; 3278 CN;
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APPLICATION NUMBER: 616,488
FILING DATE: 08-MAY-1985
APPLICATION NUMBER: 602,117
FILING DATE: 09-APR-1984
                                    FILING DATE: 09-APR-1984
APPLICATION NUMBER: 616,488
FILING DATE: 01-JUN-1984
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Best Local Similarity 100.0%;
Matches 17; Conservative
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Best Local Similarity 100.0%;
Matches 17; Conservative
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ID 5212286-50
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5212286-39
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Pred. No. 4.72e-09;
0; Mismatches 0; Indels
                                                                                                                                                 Score 137; DB 2; Length 17;
Pred. No. 4.72e-09;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 5212286
APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M.
TILLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
PEPTIDE COMPUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M. TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR PEPTIDE COMPUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 68
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/870,795
FILING DATE: 05-UNY-1986
FILING DATE: 08-MAY-1985
FILING DATE: 08-MAY-1985
APPLICATION NUMBER: 602,117
FILING DATE: 09-APR-1984
APPLICATION NUMBER: 602,117
FILING DATE: 09-APR-1984
APPLICATION NUMBER: 616,488
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/870,795
FILING DATE: 05-JUN-1986
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LENGTH: 20
SEQUENCE 21 AA; 2168 MW; 1969 CN;
                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE 17 AA; 1728 MW; 1172 CN;
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APPLICATION NUMBER: 766,030
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                      17 amino acids
     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 100.0%;
Matches 17; Conservative
                                                                                                                                               Query Match
Best Local Similarity 100.0%;
Matches 17; Conservative
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                     LENGTH: 17 amino
TYPE: amino acid
STRANDEDNESS:
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5212286-40
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ID 5212286-30
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RESULT ID 52

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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       0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M. TITLE OF INVENTION: ATRIAL NATRIURETIC/VASSODILATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; DB 4; Len. 4.72e-09;
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Pred. No. 4.72e-09;
0; Mismatches 0
       0; Mismatches
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                                                                                                                                                                                     26 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/870,795
APPLICATION NUMBER: US/07/870,795
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 766,030
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APPLICATION NUMBER: US/08/564,259
FILING DATE: 07-AUG-1990
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Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 616,488
FILING DATE: 01-JUN-1984
SEQ ID NO:28:
LENGTH: 24
SEQUENCE 25 AA; 2783 MW; 3330 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO:16:
LENGTH: 25
CFOITENCE 27 AA; 2946 MW; 3843 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 602,117
FILING DATE: 09-APR-1984
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Best Local Similarity 100.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 68
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Best Local Similarity 100.0%;
Matches 17; Conservative
  17; Conservative
                                            4 CFGGRMDRIGAQSGLGC 20
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                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                       Patent No. 5212286,
                                                                                                                                                                                                                                                                                                                                                             Patent No. 5212286
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5202239-16
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APPLICANT: KITAJIMA, YASUO
APPLICANT: FURUYA, MAYUNI
APPLICANT: MATSUO, HISAYUKI
TITLE OF INVENTION: CNP ANALOG PEPTIDES AND THEIR USE
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARRY
STREET: 1625 7
                                                                                                                                                                                                                                Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 23;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                         Score 137; DB 4;
Pred. No. 4.72e-09;
0; Mismatches 0,
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Best Local Similarity 100.0%; Pred. No. 4.72e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 AA
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APPLICATION NUMBER: US/07/828,450
FILING DATE: 19920131
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ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: 9437
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3067
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ENCE 23 AA; 2415 MW; 2174 CN;
                                                                                                                                                         LENGTH: 23
SEQUENCE 25 AA; 2772 MW; 3366 CN;
                                        APPLICATION NUMBER: 602,117
FILING DATE: 09-APR-1984
APPLICATION NUMBER: 616,488
FILING DATE: 01-JUN-1984
JMBER: 766,030
08-MAY-1985
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
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Best Local Similarity 100.0%;
Matches 17; Conservative
APPLICATION NUMBER:
FILING DATE: 08-MAY-
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GENERAL INFORMATION:
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US-07-828-450-3
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Patent No. 5204327
APPLICANT: KIYOTA, TAKAO; SUGAWARA, SHUICHI; HAYASHI, HIROSHI
TITLE OF INVENTION: TREATMENT OF CEREBRAL EDEMA WITH ANP
                                                                                                                                                                        APPLICANT: MINAMÍTAKE, YOSHIHARU
APPLICANT: KITAJÍMA, YASUO
APPLICANT: FURUYA, MAYUMI
APPLICANT: FURUYA, MAYUMI
APPLICANT: MATSUO, HISAYUKI
TITLE OF INVENTION: CNP ANALOG PEPTIDES AND THEIR USE
CORRESPONDENCE: 42
CORRESPONDENCE ADÓRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patchtin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/828,450 FILING DATE: 19920131 CLASSIFTAMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                       Sequence
Patent No. 543412
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MINAMITAKE, YOSHIHARU
APPLICANT: MINAMITAKE, YOSHIHARU
KITAJIKA, YASUO
                                                                                                   Sequence 4, Application US/07828450
                                                              Sequence 4, Application US/07828450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
SEQUENCE 27 AA; 2838 MW; 3351 CN;
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NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26.5
REFERENCE/DOCKET NUMBER:
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CURRENT APPLICATION DATA:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity, 100.0%;
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                 CITY: WASHINGTON
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                             USA
20036
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5204327-1
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APPLICANT: TARNOWSKI, JOSEPH S.;HILLIKER, SANDRA; WILLETT,
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                                                                                                                                                                                                             APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M. TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR PEPTIDE COMPUNDS
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Pred. No. 4.72e-09;
0; Mismatches 0
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                                                   27 AA.
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APPLICATION NUMBER: US/08/564,259
FILING DATE: 07-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29 AA
                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 68
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/870,795
FILING DATE: 05-JUN-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 766,030
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                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 09-APR-1984
APPLICATION NUMBER: 616,488
FILING DATE: 01-JUN-1984
                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 08-MAY-1985 APPLICATION NUMBER: 602,
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Best Local Similarity 100.0%;
Matches 17; Conservative
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                                                     STANDARD;
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                                                                                                                                                           Patent No. 5212286
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ID US-07-828-450-4
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LENGTH: 25
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                                     RESULT 9
ID 5212286-27
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ID 5202239-5
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Best Local S
Matches 1
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Length 27; 0; Indels

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Gaps
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Patent No. 5352770

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: PORCINE DERIVED NOVEL PHYSIOLOGICALLY

TITLE OF INVENTION: ACTIVE PEPTIDE

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSÉE: CUSHMAN, DARBY & CUSHMAN
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                                                                                                                                                                           Length 28;
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Pred. No. 4.72e-09;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
RPLING DATE: 19921220
                                                                                                                                                                      Score 137; DB 4; I
Pred. No. 4.72e-09;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                     28 AA.
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ATTORNEY/ACENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: 9437
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3067
TELEFRAX: 202-822-0944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/07778847
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JENCE 28 AA; 3018 MW; 3624 CN;
                                                                                                   LENGTH: 28
NCE 30 AA; 3303 MW; 4581 CN;
                             APPLICATION NUMBER: 100,144
FILING DATE: 28-AUG-1987
SEQ ID NO:2:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.0%;
Matches 17; Conservative
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Best Local Similarity 100.0%;
Matches 17; Conservative
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STATE: D.
COUNTRY:
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US-07-778-847-1
                                                                                                                            SEQUENCE
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APPLICANT: Forssmann, Wolf-Georg; Gagelmann, Michael; Hock, Dieter TITLE OF INVENTION: PHOSPHORYLATED DERIVATIVES OF CARDIODILATIN/AND PEPTIDES
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C APPLICANT: FORSSMANN, WOLF-GEORG;ALT, JEANETTE M.;BECKER,
C ERHARD; BTERBEY. FRANZ
C TITLE OF INVENTION: CARDIODILATIN FRAGMENT, PROCESS FOR
NUMBER OF SEQUENCES: 4

C CURRENT APPLICATION DATA:
C APPLICATION NUMBER: US/08/185,240
FILING DATE: 24-JAN-1994
C FILING DATE: 16-DEC-1992
C APPLICATION NUMBER: 994,084
FILING DATE: 16-DEC-1992
C FILING DATE: 16-DEC-1992
C APPLICATION NUMBER: 494,084
FILING DATE: 16-DEC-1992
C APPLICATION NUMBER: 494,084
FILING DATE: 16-DEC-1992
C APPLICATION NUMBER: 401,401
FILING DATE: 01-SEP-1989
                                                                                                                                                                      Score 137; DB 4; Length 28; Pred. No. 4.72e-09;
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Pred. No. 4.72e-09;
0; Mismatches 0
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/95,049
FILING DATE: 22-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 499,251
FILING DATE: 10-MAY-1990
APPLICATION NUMBER: US/07/435,659
FILING DATE: 13-NOV-1989
SEQ ID NO:1:
                                                                                                                                                                                                                                                                                                                                                                                                                   30 AA.
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SEQUENCE 30 AA; 3303 MW; 4581 CN;
                                                                                                   TH: 28
30 AA; 3303 MW; 4581 CN;
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Best Local Similarity 100.0%;
Matches 17; Conservative
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Best Local Similarity 100.0%;
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                   LENGTH:
SEQUENCE 30
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5461142-1
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Search completed: Wed Jun 16 13:16:53 1999 Job time : 6 secs.

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C-type natriuretic peptide B natriuretic peptide t C-type natriuretic peptide t datriuretic peptide c natriuretic peptide probable translation elongation factor G (translation elongation probable fush protein translation elongation translation elongation hypothetical protein

AWHUB AWHUB A36394 A36394 S12986 A36159 A56118 A56118 A36118 A36118 A36118 A36118 C71324 C71324 C71327 C713

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24 103 75.2 25 103 75.2 26 103 75.2 27 101 73.7 29 101 73.7 31 101 73.7 32 101 73.7 33 100 73.7 34 100 73.0 35 86 62.8 36 62.8	70 65 62 63 61	RESULT 1 ENTRY TITLE ALTERNATE_NAMES ANP; atl ORGANISM #formal_DATE		#journal Blochem #fitle Structus polype cDNA. #cross-references MUII #accession A25302	##TESCIOUS TO THE PROPERTY OF	24-149 #pp 122-149 #pp 128-144 #pp 5UMMARY #length	latch real Simi real Simi reference reference 2	DATE 21-NOV-
	MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Run on: Wed Jun 16 13:14:33 1999; WasPar time 3.33 Seconds Tabular output not generated. Title: >US-09-027-777B-1 Description: (1-17) from US09027777B.pep		Post-processing: Minimum Match 0% Listing first 45 summaries Database: pir60	Statistics: Mean 27.474; Variance 37.508; scale 0.732 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution	SCORE MATCH Length DB ID Description Pr	137 100.0 149 1 AWD. atrial natriuretic per 137 100.0 150 1 AWHU natrial natriuretic per 137 100.0 151 1 AWHU natrial natriuretic per 137 100.0 152 1 AWBO atrial natriuretic per 137 100.0 153 2 S14873 atrial natriuretic per 137 100.0 161 4 155480 hypothetical natriuretic per 137 100.0 161 4 155480 hypothetical natriure 131 95.6 128 2 S14872 atrial natriuretic per 133 195.6 128 2 S14872 atrial natriuretic per 134 155480 hypothetical natriuretic per 135 1556 1556 1558 1558 1558 1558 1558 155	93.4 152 1 AWKT atrial natriuretic ra 93.4 153 1 AWRB atrial natriuretic pe 93.4 153 1 AWRB atrial natriuretic pe 86.1 30 2 501657 atrial natriuretic pe 81.8 2 516947 atrial natriuretic pe 80.3 27 2 A3331 ventricular natriuretic pe 77.4 37 2 571382 lebetin 2 isoform bet 77.4 103 2 A41403 aldoseterone secretion 77.4 103 2 A41403 brain natriuretic pe 77.4 103 2 A41403 brain natriuretic pe 77.4 105 2 B57381 peptin 2 isoform alp 77.4 105 2 B57382 natriuretic peptide t 77.4 115 2 515822 natriuretic peptide t 77.4 131 2 A33873 brain natriuretic peptide t	100 7.4 131 2 A31070 Drain marriuretic fac 2.4 104 75.9 22 2 JT0581 matriuretic peptide t 7.4

ALIGNMENTS

NAMES	AWDG #tvpe complete
RINATE_NAMES	
MSIN	atrial natriuretic peptide precursor – dog ANP: atrial natriuretic polvpeptide
	#formal_name Canis lupus familiaris.#common_name dog 12-mar-1888 #sequence_revision 31-Mar-1988 #text_change 22-7-n-1999
ACCESSIONS A:	A25302 A90119
#authors O	Oikawa, S.; Imai, M.; Inuzuka, C.; Tawaragi, Y.; Nakazato, H.: Matsuo H
#journal B: #title S:	Dischem. Blophys. Res. Commun. (1985) 132:892-899 Structure of dog and rabbit precursors of atrial natriuretic polypeptides deduced from nucleotide sequence of cloned
#cross-reference	#cross-references MulD:86076957
#accession A25302 ##molecule type mRNA	AZ530Z
##residues	1-149 ##label OIK
##CIOSS-refer	##cross-references GB:M12045; NID:g163900; PID:g163901 FTCATION femorfamily matriaretic mentide a precured
	atrium; diuretic; hormone; natriuretic; osmoregulation
1-23 24-149	#domain signal sequence #status predicted #label SIG\ #product gamma atrial natriuretic factor #status
122-149	<pre>predicted #label ANF\ #product alpha atrial natriuretic peptide #status</pre>
128-144	<pre>predicted #label ANP\ #disulfide bonds #status predicted</pre>
	#length 149 #molecular-weight 15819 #checksum 8040
Query Match Best Local Simil. Matches 17;	100.0%; Score 137; DB 1; Length 149; Similarity 100.0%; Pred. No. 4.27e-18; 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 128 CFGGRMDRIGAQSGLGC	GAQSGLGC 144
Qy 1 CFGGRMDR	CFGGRMDRIGAQSGLGC 17
. 7	\$13107 #type complete
TITLE a	atrial natriuretic peptide precursor - pig
ORGANISM #	factor (california) #formal_name Sus scrofa domestica #common_name domestic plg 21-Nov-1993 #sequence revision 14-7m1-1994 #faxt change

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##molecule_type DNA
##residues 1-75 ##label RE3
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natriuretic peptide A precursor - human
ANF; atrial natriuretic factor; atrial natriuretic protein;
prepronatriodilatin (PND)
atrial alpha natriuretic peptide (ANP); cardiodilatin (atrial
agamma natriuretic peptide (ANP); cardiodilatin (atrial
gamma natriuretic factor)
formal_name Homo sapiens #common_name man
15-Nov-1984 #sequence_revision 15-Nov-1984 #text_change
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Nature (1984) 312:654-656
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20-Mar-1998
S13107: A60899
S13107: A60899
ERENCE
S13107
Maggert, H.J.; Appelhans, H.; Gassen, H.G.; Forssmann, W.G.
#journal Nuclect Acids Res. (1990) 18:6704
#title Nuclectide sequence of a porcine prepro atrial natriuretic peptide (ANP) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #domain signal sequence #status predicted #label SIG\
#product gamma atrial natriuretic factor #status
predicted #label ANF\
#product alpha atrial natriuretic peptide #status
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allelic variant with UGA termination codon replaced
CGA arginine codon
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Oikawa, S.; Imai, M.; Ueno, A.; Tanaka, S.; Noguchi, T.;
Nakazato, H.; Kangawa, K.; Fukuda, A.; Matsuo, H.
                                                                                                                                                                                                                                       Forssmann, W.G.; Hock, D.; Lottspeich, A.; Henschen, A.; Kreye, V.; Christmann, M.; Reinecke, M.; Metz, J.; Carlquist, M.; Mutt., V.
Anat. Embryol. (1983) 168:307-313
The right auxicle of the heart is an endocrine organ. Cardiodilatin as a peptide hormone candidate.
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I39458; I39459; I39460; I37167
                                                                                                                                                                                                                                                                                                                                                                                                  ##molecule_type protein
##residues 25-54 ##label FOR
FICATION #superfeatly natriuretic peptide A precursor
ADS atrium; diuretic; hormone; natriuretic; osmoregulation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                predicted #label ANP\
#disulfide_bonds #status predicted
#length 150 #molecular-weight 16351 #checksum
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Pred. No. 4.27e-18;
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Best Local Similarity 100.0%;
Matches 17; Conservative
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#authors Kangawa, K.; Matsuo, H.
#journal Blochem. Blophys. Res. Commun. (1984) 118:131-139
#title Burification and complete amino acid sequence of alpha-human
atrial natriuretic polypeptide (alpha-hANP).
#cross-references MUID:84128019
#accession A32733
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#journal Biochem. Biophys. Res. Commun. (1984) 125:797-802
#title Cloning of genomic DNA for human atrial natriuretic factor.
#cross_references WIID:85096983
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#journal Eur. J. Biochem. (1991) 196:281-286
#title Hydrolysis of intact and Cys-Phe-cleaved human atrial
matriuretic peptide in vitro by human tissue kallikrein.
#cross-references MUID:51176998
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$fournal Science (1984) 226:1206-1209

#title Nucleotide sequences of the human and mouse atrial nationaria factor genes.

#cross-references_MUID:85065766
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##cross-references GB:K02044; NID:9178631; PID:9178632
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##residues 1-151 ##label RES
##cross-references GE:M30262; NID:g180181; PID:g180182
874E S14097
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##residues 1-151 ##label OIK
##cross-references GB:K02043; NID:g178629; PID:g178630
NNCE A29370
#journal Nature (1984) 309:724-726
#title Cloning and sequence analysis of CDNA encocan for human atrial natriuretic polypeptide.
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##residues 1-64,'D',66-151 ##label SEI
##cross-references GB:K02043
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#accession 158054
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Homcy, C.J.; Duby, A.D.; Choi, E.; Graham, R.M.; Seidman,
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#product cardiodilantin #status predicted #label CDD\
#product atrial alpha natriuretic peptide #status
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#length 151 #molecular-weight 16395 #checksum 3644
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Life Sci. (1986) 381:3109-1315
Purification and sequence determination of bovine atrial
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#journal Biochem. Biophys. Res. Commun. (1986) 136:396-403
#fitle Structure and analysis of the bovine atrial natriuretic peptide precursor gene.
#cross-references WUD:86215205
                                                                                               Hypertension (1985) 7:31-34
Molecular studies of the atrial natriuretic factor gene.
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ANP; atrial natriuretic polypeptide
#formal_name Bos primigenius taurus #common_name cattle
30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change
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Journal Nature (1984) 312:656-658

#fitle Nuclectide sequence of the gene encoding human atrial natriuretic factor precursor.
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##cross-references EMBL:X01471; NID:g28690
T Cardiodilantin is a vasoconstrictor but not a diuretic
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High level expression of alpha-human atrial natriuretic factor as a fusion polypeptide with phage fr coat protein in Escherichia coli.
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#product gamma atrial natriuretic factor #status
predicted #label ANRN
#product alpha atrial natriuretic peptide #status
experimental #label ANRN
#disulfide_bonds #status predicted
#length 152 #molecular-weight 16518 #checksum 7552
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Schulz-Knappe, P.; Forssmann, W.G.
submitted to the EMBL Data Library, March 1991
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CLASSIFICATION #superfamily natriuretic peptide A precursor
SUMMARY #length 153 #molecular-weight 16825 #checksum
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Pred. No. 4.27e-18;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 137; DB 1; I
Pred. No. 4.27e-18;
0; Mismatches 0;
                                      ##molecule_type protein
##residues 123-150 ##label ONG
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##residues 1-153 ##label MAE
#cross-references MUID:86173941
#accession A93049
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Best Local Similarity 100.0%;
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Best Local Similarity 100.0%;
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#product atrial natriuretic peptide #status predicted
#label MAT\
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ANF(1-33); ANF(2-33); ANF(8-33); ANF(8-33); atrial
natriuretic peptide; atriopeptin I; atriopeptin II;
auriculin A; auriculin B; preprocardionatrin
#formal_name Rattus norvegicus #common_name Norway rat
19-Feb-1984 #sequence_revision 15-Nov-1984 #text_change
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A20973; A44190; A60390; I59094; I58057; I52678
A22570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##cross-references EMBL:X58562; NID:g49543; PID:g49544
##experimental_source heart atrita; adult
#FICATION #superfamily natriuretic peptide A precursor
DS atrium; diuretic; hormone; natriuretic; osmoregulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maegert, H.J.; Hanke, M.; Schmeding, G.; Teuteberg, Schulz-Knappe, P.; Forssmann, W.G. submitted to the EMBL Data Library, March 1991
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                                                                     ##residues______1-161 ##label RES
##cross-references GB:S6567; NID:g435742; PID:g435743
#bcross-references GB:S6567; NID:g435742; PID:g435743
fusion protein
:Y #length 161 #molecular-weight 17287 #checksum
Length 128;
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Pred. No. 4.27e-18;
...marthes 0; Indels
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##cross-references GB:K02062; NID:g202899; PID:g202900
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#length 128 #checksum 8741
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                                                                                                                                                                        Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 17; Conservative
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Best Local Similarity 94.1%;
Matches 16; Conservative
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KEYWORDS
FEATURE
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SUMMARY
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#authors Atlas, S.A.; Kleinert, H.D.; Camargo, M.J.; Januszewicz, A.; Sealey, J.E.; Laragh, J.H.; Schilling, J.W.; Lewicki, J.A.; Johnson, L.K.; Mack, T. #aack, T. #ack, J.W.; Lewicki, J.A.; #journal Nature (1984) 309:717-719 #title Purification, sequencing and synthesis of natriuretic and #cross-references MUID:84219796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seidah, N.G.; Lazure, C.; Chretien, M.; Thibault, G.; Garcia, R.; Cantin, M.; Genest, J.; Nutt, R.F.; Brady, S.F.; Lyle, T.A.; Paleveda, W.J.; Colton, C.D.; Ciccarone, T.M.; Veber,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ξ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Structure of rat atrial natriuretic factor precursor deduced
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #authors Seidman, C.E.; Duby, A.D.; Choi, E.; Graham, R.M.; Haber, Homcy, C.; Smith, J.A.; Seidman, J.G.
#journal Science (1984) 225:334-326
#title The structure of rat preproatrial natriuretic factor as defined by a complementary DNA clone.
#cross-references MIDD:84250178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #journal Science (1984) 223:67-69
#title Purification and sequence analysis of bioactive atrial peptides (atriopeptins).
#cross-references MUID:84097513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##residues 1-152 ##label MAK
##cross-references GB:X00665; EMBL:X00658; NID:955711; PID:955712
:NCE A43617
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##cross-references GB:K02062; GB:K02063; NID:g202899; PID:g202900
REFERENCE A93330
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Amino acid sequence of homologous rat atrial peptides:
natriure:ic activity of native and synthetic forms.
                                                                                                                                                                                                                                                                                                                                            Maki, M.; Takayanagi, R.; Misono, K.S.; Pandey, K.N.;
Tibbetts, C.; Inagami, T.
Nature (1984) 309:722-724
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                                                                                             cDNA for the
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##residues ___25-28.'X',30-31,'X',33,'X',35-38 ##label THI
                                                                                                                                                                                                                   ##molecule_type_mRNA
##residues 1-152 ##label YAM
##cross-references EMBL:X00665; NID:g55711; PID:g55712
:NCE A93332
Brewer, M.; Friedemann, T.; Miller, J.;
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Lazure, C.; Chretien, M.; Cantin, M.
Peptides (1988) 9:47-53
                                                                                             the
                #journal Nature (1984) 309:119-722
#title Cloning and sequence analysis of natriuretic factor precursor.
#cross_references MUID:84219797
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##residues 126-149 ##label ATL
SNCE A94275
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#cross-references MOID:84219798
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##molecule_type mRNA
##residues 1-152 ##label FLY
##residues 1-152 ##label FLY
##cross-references GB:R02062; NID:g202899; PID:g202900
##cross-references GB:R02062; NID:g202899; PID:g202900
##note part of this sequence, including the amino ends of three
mature peptides, was confirmed by protein sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #authors Gardner, D.G.; vlasuk, G.P.; Baxter, J.D.; Fiddes, J.C.;
Lewicki, J.A.
#journal Proc. Natl. Acad. Sci. U.S.A. (1987) 84:2175-2179
#title Identification of atrial natriuretic factor gene transcripts
in the central nervous system of the rat.
#cross-references MUID:87175636
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Identification of rat gamma atrial natriuretic polypeptide
and characterization of the cDNA encoding its precursor.
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Purification of rat pro-atrial narriurelic factor: a simplified scheme using reversed-phase high-performance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kangawa, K.; Tawaragi, Y.; Oikawa, S.; Mizuno, A.;
Sakuragawa, Y.; Nakazato, H.; Fukuda, A.; Minamino, N.;
                                                                                 A44190 Flynn, T.G.; Davies, P.L.; Kennedy, B.P.; de Bold, M.L.; Bold, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Flynn, T.G. Can. J. Physiol. Pharmacol. (1987) 65:2013-2020 the elucidation of the structure of atrial natriuretic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *superfamily natriuretic peptide A precursor atrium; diuretic; hormone; natriuretic; osmoregulation
                                                                                                                                                                                                      DNA
                                                                                                                                                   #journal Science (1985) 228:323-325
#title Alignment of rat cardionatrin sequences with the preprocardionatrin sequence from complementary #cross-references MUID:85168263
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##moleule_type mRNA
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##molecule_type mRNA
##residues 3 MB-152 ##label RES
##cross-references GB-MIS868; NID:9202903; PID:9202904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 factor, a new peptide hormone.
#cross-references MUID:88109092
                                     ##molecule_type protein
##residues 118-150 ##label SE2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             liquid chromatography.
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159094
across-references MUID:84194062
accession A20973
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#product ANF(2-33) #status experimental #label ANF2\
#product ANF(3-33) #status experimental #label ANF3\
#product cardionatrin I #status experimental #label CNI\
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#product auriculin B #status experimental #label ANF4\
#product auriculin A #status experimental #label ANB\
#product auriculin A #status experimental #label ANB\
#product auriculin A #status experimental #label ANB\
#product atrial natriuretic factor #status predicted
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#product atriopeptin II #status experimental #label AT2\
#disulfide_bonds #status experimental
#length 152 #molecular-weight 16556 #checksum 7818
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#product pro-atrial natriuretic factor #status
experimental #label PRO\
#product cardionatrin IV #status experimental #label
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#formal_name Mus musculus #common_name house mouse
31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change
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#length 152 #molecular-weight 16645 #checksum 9384
                                                                                                                             product ANF(1-33) #status experimental #label
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#title Nucleotide sequences of the human and mouse atrial natriuretic factor genes.
#cross-references MUID:85065766
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Seidman, C.E.; Bloch, K.D.; Klein, K.A.; Smith,
Seidman, J.G. .......
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##cross-references GB:K02781; NID:9191937; PID:9387099
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Matches 16; Conservative
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Matches 16; Conservative
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#accession

130-146 124-151

SUMMARY

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Matches

#journal #title

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natriuretic peptide-24
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#domain propeptide #status predicted #label PRO\
#product atrial natriuretic peptide-24 #status
experimental #label M24\
#product atrial natriuretic peptide-21 #status
experimental #label M21\
#storimental #label M21\
#disulfide_bonds #status predicted
#lasel h145 #molecular-weight 15934 #checksum 1892
                                                                                                                                                                                                                                                                                               Sakata, J.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. (1988) 155:1338-1345
Identification of new atrial natriuretic peptides in frog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ventricular natriuretic peptide - Japanese eel #formal_name Anguilla japonica #common_name Japanese eel 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Dec-1994
ANP; atrial natriuretic factor (ANF)
atrial natriuretic peptide-21; atrial natriuretic peptid
#formal_name Rana catesbeiana #common_name bullfrog
30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change
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A novel natriuretic peptide isolated from eel cardiac
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##residues 122-145 ##label SAK
%T In mammals, several active peptides may be derived from the
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Pred. No. 8.56e-12;
1; Mismatches 2; Indels
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#superfamily natriuretic peptide A precursor
#length 36 #molecular-weight 3941 #checksu
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submitted to JIPID, May 1991
JQ0947
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#accession S15821
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#accession A31510
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Best Local Similarity 82.4%;
Matches 14; Conservative
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                                                                                                                                             H.; Matsuo, H. State Commun. (1985) 132:892-899
Structure of dog and rabbit precursors of atrial natriuretic polypeptides deduced from nucleotide sequence of cloned CDNA.
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Olkawa, S.; Imai, M.; Inuzuka, C.; Tawaragi, Y.; Nakazato.
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FEBS Lett. (1988) 238:300-306
The amino acid sequences of frog heart atrial
natriuretic-like peptide and mammalian ANF are closely
           #formal_name Oryctolagus cuniculus #common_name domestic
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#formal_name Rana ridibunda #common_name laughing frog
01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change
09-Dec-1994
801657; A30977
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                                     31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 20-Mar-1998
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KEYWORDS atrium; diuretic; hormone; natriuretic; osmoregulation
FEATURE
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predicted *labal ANR'
*product alpha atrial natriuretic peptide *status
*predicted *label ANP\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S01657 #type fragment atrial natriuretic factor - laughing frog (fragment)
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#length 153 #molecular-weight 16843 #checksum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 128; DB 1; Length 153;
Pred. No. 8.63e-16;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 30;
                                                                                                                                                                                                                                                                                                                       ##molecule_type mRNA
##residues 1-153 ##label OIK
##cross-references GB:M12046; NID:9164770; PID:9164771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 118; DB 2; I
Pred. No. 2.82e-13;
3; Mismatches 0;
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##residues 1-30 ##label LAZ
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#cross-references MUID:89005705
                                                                                                                                                                                                                                                                             #cross-references MUID:86076957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 94.1%;
Matches 16; Conservative
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Best Local Similarity 82.4%;
Matches 14; Conservative
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#authors

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Gaps

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#formal_name Sus scrofa domestica #common_name domestic pig
#77-Aug-1995 #sequence_revision 19-Oct-1995 #text_change
16-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D....
The translation of the start codon ATG is not given in
this paper
                                                                                                                                                                #authors Takei, Y.; Takahashi, A.; Watanabe, T.X.; Nakajima, K.; Sakakibara, S. Sakakibara, S. Biochem. Biophs. Res. Commun. (1989) 164:537-543 #title Amino acid sequence and relative biological activity of eel atrial narriuretic peptide. #Cross-references MUD:90026430 #accession A33431
A33431 #type complete
atrial natriuretic factor - Japanese eel
#formal_name Anguilla japonica #common_name Japanese eel
27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change
09-Dec-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bnp
#superfamily natriuretic peptide A precursor
brain; natriuretic
#slength 27 #molecular-weight 3002 #checksum 9351
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#length 27 #molecular-weight 2792 #checksum 8900
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Pred. No. 2.64e-11;
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                                                                                                                                                                                                                                                                                         ##status preliminary
##molecule_type protein
##molecule_type protein
##racidues 1-27 ##label TAK
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Best Local Similarity 76.5%;
Matches 13; Conservative
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Best Local Similarity 76.5%;
Matches 13; Conservative
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##residues 1-27
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ELONGATION FACTOR G, M HYPOTHETICAL 30.8 KD P HYPOTHETICAL 46.5 KD P ELONGATION FACTOR G (E

PROTO-ONCOGENE

VAV_HUMAN

C-TYPE NATRIURETIC PEP
ATRIAL NATRIURETIC PEP
BRAIN NATRIURETIC PEP
BLONGATION FACTOR G (E
ELONGATION FACTOR G (E
ELONGA

ANFC_HUMAN
ANFC_MOUSE
ANFC_MOUSE
ANFC_RAT
ANFC_RAT
ANFC_ANGJA
ANF_CHICK
ANFB RAT
ANFB_CHICK

126 126 126 126 126 127 129 121 121 121 121 121 121 124 130 140 140 140 140

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	Releas Copyri	e 3.1A John F. Collins, Biocomputing Research Unit. ght (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd		
Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd	MPsrch_pp prot	ein - protein database search, using Smith-Waterman algorithm		44.
	Run on:	Wed Jun 16 13:15:10 1999; MasPar time 2.30 Seconds 208.756 Million cell updates/sec		444
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Re Co Ltp	Sequence:	137 1 CFGGRMDRIGAQSGLGC 17	RE	Sur
Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd protein - protein database search, using Smith-Waterman algorithm Wed Jun 16 13:15:10 1999; MasPar time 2.30 Seconds 208.756 Million cell updates/sec 1 CNS-09-027-777B-1 >US-09-027-777B-1 COTE: 137 COTE: 137	Scoring table:	РАМ 150 Gap 15	AC	
Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd protein - protein database search, using Smith-Waterman algorithm Wed Jun 16 13:15:10 1999; MasPar time 2.30 Seconds Wed Jun 16 13:15:10 1999; MasPar time 2.30 Seconds 1 CNS-09-027-777B-1 >US-09-027-777B-1 CNS-09-027-777B-1	Searched:	77977 seqs, 28268293 residues		
Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd protein - protein database search, using Smith-Waterman algorithm Wed Jun 16 13:15:10 1999; MasPar time 2.30 Seconds 1tput not generated. >USB.756 Million cell updates/sec >USB.756 Million cell updates/sec 1.17 from US09027777B.pep 1.17 from US09027777B.pep 1.17 from US09027777B.pep 1.18 from US09027777B.pep 1.17 from US09027777B.pep 1.18 from US09027777B.pep	processing:	Minimum Match 0% Listing first 45 summaries	8 8 6	
Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd protein - protein database search, using Smith-Waterman algorithm Wed Jun 16 13:15:10 1999; MasPar time 2.30 Seconds 1tput not generated. >USB.756 Million cell updates/sec 1.17) from US09027777B.ppp 1.17) from US09027777B.ppp 1.17) from US09027777B.ppp 1.18	Database:	<pre>swiss-prot37 1:swissprot</pre>	888	
Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd protein - protein database search, using Smith-Waterman algorithm Wed Jun 16 13:15:10 1999; MasPar time 2.30 Seconds 1tput not generated. >US09 -027 - 777B - 1 >US09 -09 -027 - 777B - 1 >US09 -09 -09 -09 -09 -09 -09 -09 -09 -09	Statistics:	Mean 28.233; Variance 33.694; scale 0.838	A A	
Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd protein - protein database search, using Smith-Waterman algorithm Wed Jun 16 13:15:10 1999; MasPar time 2.30 Seconds 208.756 Million cell updates/sec tiput not generated. >US-09-027-777B-1 >US-09-027-777B-1 >US-09-027-777B-1 (1-17) from US09027777B.pep CFGRWDRIGAQSGLGC 17 CFGRWDRIGAQSGLGC 17 LFGGRWDRIGAQSGLGC 17 LFGGRWDRIGAGSGLGC 17 LFGGRWDRIGAGSGLGC 17 Sep 15 77977 seqs, 28268293 residues Sssing: Minnimum Match O% Listing first 45 summaries Swiss-prot37 Liswissprot Swiss-prot33; Variance 33.694; scale 0.838	Pred. No. score grea and is der	is the number of results predicted by chance to have a ter than or equal to the score of the result being printed, ived by analysis of the total score distribution.	RRRR	
Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd protein - protein database search, using Smith-Waterman algorithm Wed Jun 16 13:15:10 1999; MasPar time 2.30 Seconds 208.756 Million cell updates/sec DI: (1-17) from US09027777B.pep 207e: 137 1 CFGGRMDRIGAQSGLGC 17 I CFGGRMDRIGAQSGLGC 17 I CFGGRMDRIGAQSGLGC 17 I Season 150 Gap 15 77977 seqs, 28268293 residues Swiss-prot37 1:swissprot 1:swissprot Swiss-prot37 1:swissprot 1:swissprot 1:swissprot 1:swissprot 1:swissprot 2: Mean 28.233; Variance 33.694; scale 0.838 1:wo. is the number of results predicted by chance to have a re greater than or equal to the score of the result being printed, is derived by analysis of the total score distribution.			₹	

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ 01-APR-1988 (REL. 07, CREATED) 01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE) 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE) ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE) ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP) (ANP) (PREPRONATRIODILATIN).
NPPA.
CANIS FAMILIARIS (DOG).
CHRAXOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
CARNIVORA; FISSIPEDIA; CANIDAE; CANIS. Length 149 Score 137; DB 1; Pred. No. 7.24e-21; 0; Mismatches 0 149 AA; 15819 MW; D4F3A6CF CRC32; Æ PIR; A25302; AWDG.
PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
PEM: PF00212; ANP; 1.
VASCACTIVE; SICNAL.
SIGNAL. entities requires a license agreement (Se or send an email to license@isb-sib.ch). ALIGNMENTS PRT; Query Match
Best Local Similarity 100.0%;
Matches 17; Conservative EMBL; M12045; G163901; JT I ANF_CANFA P07499; PEPTIDE DISULFID SEQUENCE STITE BORRERS SOLUTION OF THE SOLUTION OF THE

7.24e-21 7.24e-21 7.24e-21 7.24e-21 7.24e-21 4.05e-19 2.98e-18 2.98e-18 2.98e-18 2.98e-18

Description

DB

Query Match

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ANF_BOUIN
ANF_BOUSE
ANF_CAVPO
ANF_RAT
ANF_RAT
ANF_RANCI
ANF_RESC
ANF_CIRISC

ANFC_SQUAC ANFC_SHEEP

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Gaps

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0; Indels

152 AA

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01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
                                                                                                                                                                                                                                                                                                                                  "purification and sequence determination of bovine atrial natriuretic factor.";
                                                                                                                                                                                                                                                                                           MEDLINE; 86173941.
ONG H., MCNICOLL N., LAZURE C., SEIDAH N., CHRETIEN M., CANTIN M.,
DE LEAN A.;
                                                                                                                                                                                                       VIASOR G.P., MILLER J., BENCEN G.H., LEWICKI J.A.; "Structure and analysis of the bovine atrial natriuretic peptide precursor gene.";
                                                                                                                         BOS TAURUS (BOVINE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
ARTIODACTYLA; RUMINANTIA; PECORA; BOVOIDEA; BOVIDAE; BOVINAE;
                                                                                                                                                                                                                                                BIOCHEM. BIOPHYS. RES. COMMUN. 136:396-403(1986)
                                        (REL. 07, CREATED)
                                                                                           (ANP) (PREPRONATRIODILATIN).
           STANDARD;
                                                                                                                                                                                                                                                                             SEQUENCE OF 123-150.
                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 86215205.
        ANF_BOVIN
P07501;
01-APR-1988
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                                                                                                                            01-MAR-1992 (REL. 21, CREATED)
01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
ATELAL MATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
(ANP) (PREPRONATRIODILATIN)
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 25-150.
TISSUE-HEART RIGHT ATRIUM;
MEDLINE: 85124561.
FORSSMANN W.G., BIRR C., CARLOUIST M., CHRISTWANN M., FINKE R.,
HENSCHEN A., HOCK D., KIRCHHEIM H., KREYE V., LOTTSPEICH F., METZ J.,
MUTT V., REINECKE M.,
"The auxicular myocardiocytes of the heart constitute an endocrine organ. Characterization of a porcine cardiac peptide hormone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BY SIMILARITY).
ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cardiodilatin-126.";
CELL TISSUE RES. 238:425-430(1984).
-!- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE
SUBSTANCE SYNTHESIZED IN WANMALLAN ATRIA AND IS THOUGHT TO PLAY A
KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
                                                                                                                                                                                                                                                                  -!- A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARDIODILATIN-RELATED PEPTIDE (CDP)
                                                                                                                                                                                                                         EUKARYOTA; METAŽOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
ARTIODACTYLA; SUIFORMES; SUINA; SUIDAE; SUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 137; DB 1; Length 150;
Pred. No. 7.24e-21;
0; Mismatches 0; Indels
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                                                                                                   150 AA.
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PROSITE: PS00263: NATRIURETIC_PEPTIDE; 1.
PFAM: PF00212; ANP: 1.
VASOACTIVE: SIGNAL.
SIGNAL
                                                                                                                                                                                                                                                                                                                                         (ANP) CDNA.";
NUCLEIC ACIDS RES. 18:6704-6704(1990)
                                                                                                   PRT;
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Best Local Similarity 100.0%;
Matches 17; Conservative
                128 CFGGRMDRIGAQSGLGC 144
                              1 CFGGRMDRIGAQSGLGC 17
                                                                                                   STANDARD;
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                                                                                                                                                                                                               SCROFA (PIG)
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DISULFID
SEQUENCE
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ANF_PIG
P24259;
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17.5 AB
LIFE SCI. 38:1309-1315(1986).
-!- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE
SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
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                                                                                                                                                          KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
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PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
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129 145
152 AA; 16518 MW; CF200882 CRC32;
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PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
PFAM; PF00212; ANP; 1.
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NPPA OR PND.
HOMO SAPIENS (HUMAN).
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Matches 17; Conservative
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Gaps

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129 CFGGRMDRIGACSGLGC 145

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OIKAWA S., IMAI M., UENO A., TANAKA S., NOGUCHI T., NAKAZATO H., KANGAWA K., FUKUDA A., MATSUO H.;
"Cloning and sequence analysis of cDNA encoding a precursor for human atrial natriuretic polypeptide.";
NATURE 309:724-726(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIVIN R.A., CONDRA J.H., DIXON R.A.F., SEIDAH N.G., CHRETIEN M., NEMER M., CHANBERLAND M., DROUIN J.:
"Molecular cloning and characterization of DNA sequences encoding rat and human atrial natriurelic factors.";
PROC. NATL. ACAD. SCI. U.S.A. 81:6325-6329(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 94318633.

FAIRBROTHER W.J., MCDOWELL R.S., CUNNINGHAM B.C.;
"Solution conformation of an atrial natriuretic peptide variant selective for the type A receptor.";
BIOCHEMISTRY 33:8897-8904(1994).

-i- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence of the gene encoding human atrial natriuretic
                                                                                                                                                                                                                                                                                        NARATAMA K., OHKUBO H., HIROSE T., INAYAMA S., NAKANISHI S.;
"MRNA Sequence for human cardiodilatin-atrial natriuretic factor
precursor and regulation of precursor mRNA in rat atria.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEIDMAN C.E., BLOCH K.D., KLEIN K.A., SMITH J.A., SEIDMAN J.G., "Nucleotide sequences of the human and mouse atrial natriuretic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAKI M., PARMENTIER M., INAGAMI T.; "Cloning of genomic DNA for human atrial natriuretic factor."; BIOCHEM. BIOPHYS. RES. COMMUN. 125:797-802(1984).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GREENBERG B.D., BENCEN G.H., SEILHAMER J.J., LEWICKI J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NEMER M., CHAMBERLAND M., SIROIS D., ARGENTIN S., DROUIN DIXON R.A.F., ZIVIN R.A., CONDRA J.H.; "Gene structure of human cardiac hormone precursor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBMITTED (MAY-1998) TO EMBL/GENBANK/DDBJ DATA BANKS
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BIOCHEM. BIOPHYS. RES. COMMUN. 118:131-139(1984).
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SEQUENCE OF 1-151 FROM N.A.
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NATURE 312:654-656(1984).
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NATURE 312:656-658(1984).
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KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING

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01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC.PEPTIDE)
               THE HUMANI GENOME CONTAINS 2 DIFFERENT PREPRONATRIODILATIN GENES ONE CODES; FOR 2 ARG RESIDUES AT THE C-TERMINUS THAT ARE CLEAVED TO FORM THE MATURE PEPTIDE, WHILE THE OTHER ENDS IN A TERMINATION CODON IMMEDIATELY AFTER THE LAST CODON OF THE MATURE PEPTIDE. SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
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TRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
BY SIMILAND AND OF THE TWO GENES).
MISSING (IN ONE OF THE TWO GENES).
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PERISSODACTYLA; EQUIDAE; EQUUS.
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SEQUENCE FROM N.A.
STRAIN-ADAMITICUS; TISSUE-HEART ATRIUM;
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105 CFGGRMDRIGAQSSLGC 121

1 CFGGRMDRIGAQSGLGC 17

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or send an email to license@isb-sib.ch).
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01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
01-AUG-1994 (REL. 34, LAST ANNOTATION UPDATE)
ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
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ATRIAL NATRIORETIC PEPTIDE, ALPHA (ANP).
BY SIMILARITY.
C2CF552D CRC32;
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ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
BY SIMILARITY.
; FESDSF4A CRC32;
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MAEGERT H.J., HANKE M., SCHMEDING G., TEUTEBERG K.,
MAEGERT H.J., HANKE M., SCHMEDING G., TEUTEBERG K.,
SCHULZ-KARPPE P., FORSSMANN W.G.;
SCHULZ-KARPPE P., FORSSMANN W.G.;
SUBMITTED (MAR-1991) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: ATRIAL NATRIUGETIC FACTOR (AND: IS A POTENT VASOACTIVE
-!- FUNCTION: ATRIAL NATRIALIAN ATRIA AND IS THOUGHT TO PLAY A
SUBSTANCE SYNTHESIZED IN MAMMALLAN ATRIA AND IS THOUGHT TO PLAY A
KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
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EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; HYSTRICOGNATHI; CAVIIDAE; CAVIA.
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Pred. No. 7.24e-21;
......+hes 0; Indels
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Pred. No. 4.05e-19;
1; Mismatches 0;
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PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
PFAM; PF00212; ANP; 1.
                                                                                                                                                                                                                   PIR; S14873; S14873.
PROSITE; PSO0263; NATRIURETIC_PEPTIDE; 1.
PFAM; PF00212; ANP; 1.
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Best Local Similarity 94.1%;
Matches 16; Conservative
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Best Local Similarity 100.0%;
Matches 17; Conservative
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153 AA;
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ANF_CAVPO
P27596;
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(ANP) (PREPRONATRIODILATIN) (CONTAINS: AURICULINS; ATRIOPEPTINS)
                                         13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
ATRIAL NATRIURTIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
                                                                                                                                                                                                                                                                                            ENNCE 640.1200-1203(1203)

FUNCTION: ATRIAL NÀTRIDREIC FACTOR (ANF) IS A POTENT VASOACTIVE
SUBSTANCE SYNTHESIŽED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY P
KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
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                                                                                                                                                                                                                                  SEIDWAN C.E., BLOCH K.D., KLEIN K.A., SMITH J.A., SEIDWAN J.G.; "Nucleotide sequences of the human and mouse atrial natriuretic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                    MUS MUSCULUS (MOUSE).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI: MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AURICULIN A (BY SIMILARITY).
AURICULIN B (BY SIMILARITY).
ATRIOPEPTIN I (BY SIMILARITY).
ATRIOPEPTIN II (BY SIMILARITY).
BY SIMILARITY.
W; 5163CB23 CRC32;
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Pred. No. 2
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PFAM; PF00212; ANP; 1.
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94.1%;
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SCIENCE 226:1206-1209(1984)
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RATTUS NORVEGICUS (RAT).
                STANDARD;
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Best Local Similarity '
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126
127
127
129
152 AA;
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NPPA OR PND
                ANF_MOUSE
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ATLAS S.A., KLEINERT H.D., CAMARGO M.J., JANUSZEWICZ A., SEALEY J.E., LARAGH J.H., SCHILLING J.W., LEWICKI J.A., JOHNSON L.K., MAACK T.; "Purification, sequencing and synthesis of natriuretic and vasoactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZITIN R.A., CONDRA J.H., DIXON R.A.F., SEIDAH N.G., CHRETIEN M., NEMER M., CHAMBERLAND M., DROUIN J.; "Molecular cloning and characterization of DNA sequences encoding rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The elucidation of the structure of atrial natriuretic factor, a new
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 84250178.
SEIDMAN C.E., DUBY A.D., CHOI E., GRAHAM R.M., HABER E., HOMCY C., SIIDMAN J.G., SIDMAN J.G., SIDMAN J.G., The structure of rat preproatrial natriuretic factor as defined by complementary DNA clone."; SCIENCE 225:324-326(1984).
                                                                                                                                                                                                                                                                                                                                          Structure of rat atrial natriuretic factor precursor deduced from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 87175636.
GARDNER D.G., VLASUK G.P., BAXTER J.D., FIDDES J.C., LEWICKI J.A.:
"Identification of atrial natriuretic factor gene transcripts in central nervous system of the rat.";
PROC. NATL. ACAD. SCI. U.S.A. 84:2175-2179(1987).
                                                                                                       YAMANAKA M., GREENBERG B., JOHNSON L., SEILHAMER J.J., BREWER M., FRIEDEMANN T., MILLER J., ATLAS S.A., LARAGH J., LEWICKI J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KANGAWA'K., TAWARAGI Y., OIKAWA S., MIZUNO A., SAKURAGAWA Y., MAKAZATO H., FUKUDA A., MINAMINO N., MATSUO H.; "Identification of rat gamma atrial natriuretic polypeptide and characterization of the cDNA encoding its precursor.";
                                                                                                                                                                "Cloning and sequence analysis of the cDNA for the rat atrial natriuretic factor precursor.";
NATURE 309:719-722(1984).
                                                                                                                                                                                                                                                                                                   TAKAYANAGI R., MISONO K.S., PANDEY K.N., TIBBETTS C.,
MAMMALIA; EUTHERIA;
RATTUS.
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MEDLIN: 85182558.
ARGENTIN: S., NEMER M., DROUIN J., SCOTT G.K., KENNEDY
DAVIES P.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and human atrial natriuretic factors.";
PROC. NATL. ACAD. SCI. U.S.A. 81:6325-6329(1984).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The gene for rat atrial natriuretic factor."; J BIOL. CHEM. 260:4568-4571(1985).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE;
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NATURE 309:717-719(1984).
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                                                               FROM N.A.
84219797.
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SEQUENCE FROM N.A.
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FLYNN T.G.;
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INAGAMI T.:
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                                                                                                                                                                                                                     SEIDAH N.G., LAZURE C., CHRETIEN M., THIBAULT G., GARCIA R., CANTIN M., GENEST J., NUTT R.F., BRADY S.F., LYLE T.A., PALEVEDA W.J., COLYON C.D., CICCARONE T.M., VEBER D.F.; "Amino acid sequence of homologous rat atrial peptides: natriuretic activity of native and synthetic forms."; PROC. NATL. ACAD. SCI. U.S.A. 81:2640-2644(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "NH2-terminal fragment of rat pro-atrial natriuretic factor in the circulation: identification, radioimmunoassay and half-life."; PEPTIDES 9:47-53(1988).
                                        CURRIE M.G., GELLER D.M., COLE B.R., SIEGEL N.R., FOK K.F., ADAMS S.P., EUBANKS S.R., GALLUPPI G.R., NEEDLEMAN P.; "Purification and sequence analysis of bioactive atrial peptides
                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 88203350.
THIBAULT G., MURTHY K.K., GUTKOMSKA J., SEIDAH N.G., LAZURE C., CHRETIEN M., CANTIN M.;
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Pred. No. 2.98e-18;
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AURICULIN B.
ATRIOPEPTIN I.
ATRIOPEPTIN II.
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PFAM; PF00212; ANP; 1.
SEQUENCE OF 127-149, AND SYNTHESIS. MEDLINE: 84097513.
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larity 94.1%;
Conservative
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                                                                                                                 (atriopeptins).";
SCIENCE 223:67-69(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M27498; G202906; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147
149
150
                                                                                                                                                                                    SEQUENCE OF 118-150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 1
129 1
152 AA;
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nes 16; Conser
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                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 25-38.
                                                                                                                                                                                                         84194062
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PIR; A22570; AWRT
PIR; A44190; A441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANF_RABIT
P07500;
01-APR-1988 (
01-APR-1988 (
01-OCT-1996 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VASOACTIVE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEPTIDE
DISULFID
SEQUENCE
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14A325F7 CRC32;
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llarity 82.4%;
Conservative
3263 MW;
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                                        Query Match
Best Local Similarity 82.4%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D01043; D1001314; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CFGGRMDRIGAQSGLGC 17
                                                                                                                                                            1 CFGGRMDRIGAQSGLGC 17
                                                                                                                                  11 CFGSRIDRIGAQSGMGC 27
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Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 89025806.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
30 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-HEART,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANFV_ANGJA
P22642;
                                                                                                                                                                                                                                                 LT 11
ANF_RANCA
P18909;
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DISULFID
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  SEQUENCE
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ATRIAL NATRIURETIC FACTOR (AND) (ATRIAL NATRIURETIC PEPTIDE) (ANP).
ATRIAL NATRIURETIC FACTOR (AND) (ATRIAL NATRIURETIC PEPTIDE) (ANP).
ENANA RIDIBUNDA (LAUGHING FROG). (MARSH FROG).
EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: AMPHIBIA: BATRACHIA: ANURA;
NEOBATRACHIA; RANOIDEA; RANIDAE; RANINAE; RANA.
                                                                                                                                                                                                    OIKAWA S., IMAI M., INUZUKA C., TAWARAGI Y., NAKAZATO H., MATSUO H.;
"Structure of dog and rabbit precursors of atrial natriuretic
polypeptides deduced from nucleotide sequence of cloned cDNA.";
BIOCHEM. BIOPHES. ESC. COMMUN. 132.892-899(1985).
-: FUNCTION: ATRIAL NATRIUETIC FACTOR (ANF) IS A POTENT VASOACTIVE
SUBSTANCE SYMPHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
(ANP) (PREPRONATRIODILATIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE: 89005705...
MEDLINE: 89005705...
LAZURE C., ONG H., MCNICOLL N., NETCHITAILO P., CHRETIEN M.,
LAZURE C., ONG H., MCNICOLL N., NETCHITAILO P., CHRETIEN M.,
LAZURE C., ONG H., MCNICOLL N., NETCHITAILO P., CHRETICN M.,
The amino acid sequences of frog heart atrial natriuretic-like
peptide and mammalian ANF are closely related.";
peptide and mammalian ANF are closely related.";
-i- FUNCTION: VASOACTIVE ACTIVITY. HAS A CGMP-STIMULATING ACTIVITY.
-i- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                        A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS. SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                       ORYCTOLAGUS CUNICULUS (RABBIT).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
LAGOMORPHA; LEPORIDAE; ORYCTOLAGUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 128; DB 1; Length 153;
Pred. No. 2.98e-18;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16843 MW; 1FA4FB42 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               557; S01657.
PS00263; NATRIURETIC_PEPTIDE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; B25302; AWRB.
PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-1989 (REL. 10, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 93.4%;
Best Local Similarity 94.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 CFGGRIDRIGAQSGLGC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFGGRMDRIGAOSGLGC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M12046; G164771; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM; PF00212; ANP; 1.
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130 · 1
153 AA;
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                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 86076957.
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P09196:
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DISULFID
SEQUENCE
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1990 (REL. 16, CREATED)
01-NAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RANA CATESBEIANA (BULL FROG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA: ANURA;
NEOBATRACHIA; RANOIDEA; RANIDAE; RANINAE; RANA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SARATA J., KANGAWA K., MATSUO H.;
"Identification of new atrial natriuretic peptides in frog heart.";
BIOCHEM. BLOPHYS. RES. COMMUN. 155:1338-1345(1988).
BIOCHEM. ASSOACTIVE ACTIVITY. HAS A CGMP-STIMULATING ACTIVITY.
-: FUNCTION: VASOACTIVE ACTIVITY. HAS A CGMP-STIMULATING ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                   Gaps
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Pred. No. 2.10e-15;
3; Mismatches 0; Indels
Length 30;
                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL. ATRIAL FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBMITTED (XXX-1992) TO EMBL/GENBANK/DDBJ DATA BANKS
Score 118; DB 1;
Pred. No. 2.10e-15;
3; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15934 MW; 6A1FA352 CRC32,
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01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
01-5UD-1998 (REL. 36, LAST ANNOTATION UPDATE)
VENTRICULAR NATRIURETIC PEPTIDE (VNP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 AA
                                                                                                                                                                                                                                                                                                                                           145 AA
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PFAM; PF00212; ANP; 1.
VASOACTIVE; SIGNAL.
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MEDLINE; 89136947.

A MGUYEN T.T., LAZURE C., BABINSKI K., CHRETIEN M., ONG H., DE LEAN A.;
A MGUYEN T.T., LAZURE C., BABINSKI K., CHRETIEN M., ONG H., DE LEAN A.;
A MGOYEN CECTETION inhibitory factor: a novel neuropeptide in
bovine chromaffin cells.";
ENDOCRINOLOGY 124:1591-1593(1989).

- : FUNCTION! INHIBITES ALDOSTERONE SECRETION.

- : FUNCTION! WASOACTIVE ACTIVITY.

- : FUNCTION! WASOACTIVE ACTIVITY.

- : FUNCTION! WASOACTIVE ACTIVITY.

- : LISSUE SPECIFICITY: BRAIN AND ALSO IN ATRIA, BUT AT MUCH LOWER

- : SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.

- : SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.

- PRAM; FOROILE; A41403: A4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUZUKI R., TAKAMASHI A., TAKEI Y.;
"Different molecular forms of C-type natriuretic peptide isolated from the brash and heart of an elasmobranch, Triakis scyllia.";
J. ENDOCRINOL. 135:317-32(1992).
-i- FUNCTION: VASORELAXANT ACTIVITY. HAS A CGMP-STIMULATING ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- TISSUE SPECIFICITY: CNP-115 IS DIFFERENTIALLY PROCESSED TO PRODUCE (NP-38 AND CNP-39) IN THE HEART AND CNP-22 IN THE BRAIN.
-!- SIMILARIYY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
PROSITE; PSO(263; NATRIURETIC_PEPTIDE; 1.
  EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
ARTIODACTYLA; RUMINANTIA; PECORA; BOVOIDEA; BOVIDAE; BOS
                                                                                       MEDIINE; 90114187.

NGUYEN T.T., LAZURE C., BABINSKI K., CHRETIEN M., DE LEAN A., ONG
"PUTÍfication and primary structure of pro-aldosterone secretion
inhibitory factor from bovine adrenal chromaffin cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAMMA-BRAIN NATRIURETIC PEPTIDE.
ALDOSTERONE SECRETION INHIBITORY FA
BRAIN NATRIURETIC PEPTIDE (BNP-26).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRIAKIS SCYLLIUM (LEOPARD SHARK) (TRIAKIS SCYLLIA).
EUKARYOTA, METAZOA: CHORDATA: VERTEBRATA; CHONDRICHTHYES;
ELASMOBRANCHII; CARCHARHINIFORMES; TRIAKIDAE; TRIAKIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score luo;
Pred. No. 4.45e-12;
Pred. ....+rhes 2; Indels
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7488BCC0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW; E3823460 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
C-TYPE NATRIURETIC PEPTIDE (CNP-115).
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CNP-38.
CNP-22.
                                                                                                                                                                                      MOL. ENDOCRINOL. 3:1823-1829(1989)
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12904 MW;
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76.58;
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                                                                                                                                                                                                                                     69-103.
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78
81
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P55208;
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EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; ACTINOPTERYGII; NEOPTERYGII;
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"Amino acid sequence and relative biological activity of eel atrial
natriuretic peptide.";
BIOCHEM. BIOPHYS. RES. COMMUN. 164:537-543(1989).
-:- FUNCTION: EXHIBITS NATRIURETIC AND VASODEPRESSOR ACTIVITY. HAS I
CGMP-STIMULATING ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATRIAL NATRIURETIC FACTOR (ANF) (ATRIAL NATRIURETIC PEPTIDE) (ANP).
                                                                                       MEDLINE; 91243821.
TAKAHASHI A., WATANABE T.X., NAKAJIMA K., SAKAKIBARA S.;
"A novel natriuretic peptide isolated from eel cardiac ventricles."
FEBS LETT. 282:317-320(1991).
-!- FUNCTION: EXHIBITS NATRIURETIC AND VASODEPRESSOR ACTIVITY.
-!- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
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01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
BRAIN NATRIURETIC PEPTIDE PRECURSOR (BNP) (ALDOSTERONE SECRETION INHIBITORY FACTOR) (ASIF).
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                                                                                                                                                                                                                                                                                                                                                                                                      Length 36;
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9.97e-14;
FELEOSTEI; ANGUILLIFORMES; ANGUILLIDAE; ANGUILLA
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Pred. No. 3.56e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CA151EFA CRC32;
                                                                                                                                                                                                                                                                                                                                                     B3E8D338 CRC32;
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Pred. No. 9.97e-
1; Mismatches
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PROSITE: PS00265; NATRIURETIC_PEPTIDE; 1.
PFAM: PF00212; ANP; 1.
VASOACTIVE.
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PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
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3941 MW;
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27 AA; 2792 MW;
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Best Local Similarity 82.4%;
Matches 14; Conservative
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Best Local Similarity 76.5%;
Matches 13; Conservative
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                                                                    FISSUE-HEART VENTRICLE;
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36 AA;
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P13204;
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ANF_ANGJA
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Gaps

US-09-027-777B-1.rsp

Wed Jun 16 14:32:38 1999

Best Local Similarity 76.5%; Pred. No. 4.45e-12; Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps

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99 CFGVKLDRIGAMSGLGC 115 |||-::||||| |||||| 1 CFGGRMDRIGAQSGLGC 17

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Search completed: Wed Jun 16 13:15:17 1999 Job time : 7 secs.

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	£	ins, Biocomputing Research Unit. University of Edinburgh, U.K. its by Oxford Molecular Ltd	using Smith-Waterman algorithm	MasPar time 4.67 Seconds 198.730 Million cell updates/sec					ia 3:sp_fungi 4:sp_human mammal 7:sp_mhc 8:sp_organelle 11:sp_rodent 12:sp_unclassified virus	scale 0.765	cted by chance to have a of the result being printed, score distribution.		Description Pred. No.	ATRIAL NATRIURETIC FAC 3.71e-19 ATRIAL. NATRIURETIC PEP 3.71e-19 BRAIN NATRIURETIC PEPT 5.15e-11 BRAIN NATRIURETIC PEPT 4.04e-06 MYELOBLAST KIAA0227 (F 7.33e-01) UDP-N-ACETYLMURAMYTE-A 1.02e-00 UDP-N-ACETYLMURAMYTE-A 1.02e-00 UNKNOWN PRODUCT. 2.84e-00 UNKNOWN PRODUCT. 2.84e-00 COSMID FOBF8. 2.84e-00 ESTROGEN-RESPONSIVE FI 2.84e-00 DIHYDRODIPICOLINATE SY 4.42e-00 BIHYDRODIPICOLINATE SY 4.42e-00 ALANINE RACEMASE (EC 5 6.84e+00 CYTOCHROME P450. 6.84e+00
*	<u> </u>	Collins, Biocompi 198 University or rights by Oxford	database search,	:15:34 1999; Mas	-027-7778-1 from USO90277778 pep RMDRIGAOSGLGC 17		54579741 residues	0% 45 summaries	oacter 6:SP_ olant 14:SP_	Variance 35.212;	results predi l to the score of the total	SUMMARIES	ID Des	013766 ATRI 046540 ATRI 0265130 CARI 026511 BRAI 055086 BRAI 092623 MATRI 092623 UDP: 061510 COSN 019209 COSN 019209 COSN 019209 COSN 049355 HYPQ 049355 HYPQ 049355 HYPQ 061510 ESTI 061510 COSN 061510 ESTI 061510 ESTI 061510 ESTI 061510 ESTI 061510 COSN 061510 ESTI 061510 ESTI 061510 COSN 061510 ESTI 061510 ESTI 061510 COSN 061510 ESTI 061510 COSN 061510 COSN 061510 ESTI 061510 COSN 061510 ESTI 061510 ESTI 0615
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		Release Copyrig		÷	tion: Score: e:	table:	.; g	Post-processing	 v	ics:	Pred. No score gre and is de		Score	7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
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ORF H1777. HYPOTHETICAL 48.8 KD P 6.84 PROLINE PERMEASE (PUTP 6.84 ESTROGEN RESPONSIVE FI 6.84 TRANSCRIPTIONAL ACTIVA 6.84 HYPOTHETICAL 14.6 KD P 1 05 MO1612.12 PROTEIN (FRA 1.05 AGININE DECARBOXYLASE 1.05 POLY A POLYMERASE. 1.05 FOLY A POLYMERASE. 1.05 FOLY A POLYMERASE. 1.05 FOLY A POLYMERASE. 1.05 FROLINE DEHYDROGENASE. 1.05 RB18A-PROTEIN. 1.01 REVERSE-TRANSCRIPTASE 2.45 COS41.7. SINGRATE ASSIMILATION P 2.45 SINGRATE ASSIMILATION P 2.45	SINGLE-STRAND DNA-BIND PENICILLIN-BINDING PRO CELLULOSE SYNTHASE (FR	PRT; 151 AA. EEATED) ST SEQUENCE UPDATE) ST ANNOTATION UPDATE) URSOR. VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;	1J., SMIT J., HABER E., HOMCY C., SELDWAN J.G.; natriuretic factor gene."; TIDE; 1.	CARDIODILATIN-RELATED PEPTIDE (CDP). ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP). BY SIMILARITY. E8827DA3 CRC32;	: 137; DB 4; Length 151; No. 3.71e-19; Mismatches 0; Indels 0; Gaps 0;
05454 02553 02553 01425 01425 0153 01974 0453 0453 0443 0443 0443 0443 0443 044	053 065 065 ALI	PRT; 01, CREATED) 01, LAST SEO 09, LAST ANN R PRECURSOR.	DAE; HOMO. H K.D., ZISFEIN GRAHAM R.M., of the atrial 34(1985) 334(1985) 638; JOINED. NATRIURETIC_PEP	CARD ATRI BY S MW; E8	Score ; Pred. 0; M
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221 222 222 222 222 222 223 223 233 233		13 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	CATARRHINI; HOMIN SEQUENCE FROM N.A MEDLINE; 85206210 SERIDMAN C.E., BLO DUBY A.D., CHOI E "MOLECULAR SEUGLE "MASSELIMAN 7:31 EMBL; MASSELIMAN 7:31 EMBL; MASSELIMAN 7:31 EMBL; MSSELIMAN 7:31 PROSITE; PSOUZE3; AN VASOACTIVE; SICHAN	SIGNAL PEPTIDE PEPTIDE DISULFID SEQUENCE	Ouery Match Best Local Sin Matches 17, Matches 17, 130 CFGGR
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Length 129

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01-JUN-1998 (TREMBLREL. 06, L.
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Best Local Similarity 64.7%;
Matches 11; Conservative
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               Query Match
Best Local Similarity 76.5%;
Matches 13; Conservative
                                                                                                                                            107 CFGRRLDRIGSLSGLGC 123
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MEDLINE; 94237953.
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
ARTIODACTYLA; RUMINANTIA; PECORA; BOVOIDEA; BOVIDAE; CAPRINAE; OVIS.
ANP.
OVIS ARIES (SHEEP).
EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA; MAMMALIA; EUTHERIA:
ARTIODACTYLA: RUMINANTIA: PECORA; BOVOIDEA; BOVIDAE; CAPRINAE; OVIS.
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE F.M., ESPINER E.A., CAMERON V.A.;
SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF037466; G2708652;
PROSITE: PS002063; NATURETIC_PEPTIDE; 1.
SEQUENCE 129 AA; 14118 MW; 85DE4222 CRC32;
                                                                                                                   [1]
SEQUENCE FROM N.A.
AITKEN G.D., RAIZIS A.M., GEORGE P.M., ESPINER E.A., CAMERON V.A.;
SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF037465; G2708650; --
PROSITE: PSO053; WILLURETIC_PEPTIDE; 1.
SEQUENCE 152 AA: 16368 MW; D5360BCC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3

ID 029130

C29130

C29130

DT 01-WOV-1996 (TREMBLREL. 01, CREATED)

DT 01-WOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBLREL. 03, LAST ANNOTATION UPDATE)

DT 01-NOV-1998 (TREMBLREL. 03, LAST ANNOTATION UPDATE)

DE 01-NOV-1998 (TREMBLREL. 03, LAST ANNOTATION UPDATE)

CALOLODILATIN, ATRIAL NATRIAL NATRIAL PEPTIDE.

CEUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:

CANDENTIA: TUPAIIDAE: TUPAIA.

CANDENTIA: TUPAIIDAE: TUPAIA.

RA SCHNEIDEMANN S., MAEGERT H.J., FORSSMANN W.G.;

RA SCHNEIDEMANN S., MAEGERT H.J., FORSSMAN
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Pred. No. 3.71e-19;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                              Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PARDIGOL A.;
SUBMITTED (MAR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL. 270294; E233859; -
PROSITE: PS00063; NATRIURETIC_PEPTIDE; 1.
PFAM: PF00212; ANP: 1.
SEQUENCE 155 AA: 16860 MW; 77E8CA8B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   046541 PRELIMINARY; PRT; 129 AA.
046541 0646541.
01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
BRAIN NATRIURETIC PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                       Score 137; DB 6; I
Pred. No. 3.71e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 CFGGRMDRIGAQSGLGC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFGGRMDRIGAQSGLGC 17
                                                                                                                                                                                                                                                                                                                                                                                                                         17; Conservative
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TISSUE=VENOM GLAND;
MEDLINE; 98092299.
HO P.L., SOARES M.B., MAACK T., GIMENEZ I., PUORTO G., FURTADO M.F.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEVENTY.
STRAIN-129/SV,
MEDLINE; 97031884.
TAMURA N., OGAWA Y., YASODA A., NAKAO K.;
TAMURA N., OGAWA Y., YASODA A., NAKAO K.;
TAMURA N., OGAWA I., TASODA A., NAKAO K.;
TWO cardiac natriuretic peptide are organized in tandem in the mouse and brain natriuretic peptide) are organized in tandem in the mouse and brain natriuretic peptide) are organized in tandem in the mouse and brain natriuretic peptide) are organized in tandem in the mouse EMBL: D8.049: D10.25069;
J. MOL. CELL. CARDIOL. 28:1811-1815(1996).
EMBL: D8.049: D10.25069;
PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                      Gaps
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EUKRRYOTA, METAZOA; CHORDATA; VERTEBRATA; LEPIDOSAURIA; SQUAMATA;
SCLEROGLOSSA; SERPENTES; COLUBROIDEA; ELAPIDAE; ELAPINAE; MICRURUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OGAWA Y., ITOH H., TAMURA N., SUGA S., YOSHIMASA T., UEHIRA M., MATSUDA S., SHIONO S., NISHIMOTO H., NAKAO K.; "Molecular cloning of the complementary DNA and gene that encode mouse brain natriuretic peptide and generation of transgenic mice that overaxpress the brain natriuretic peptide gene."; J. CLIN. INVEST. 93:1911-1921(1994).
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Pred. No. 4.04e-06;
3; Mismatches 3; Indels
Score 106; DB 6; Lengtn 12>
Pred. No. 5.15e-11;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST SEQUENCE UPDATE)
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                                                                                                                                                                                                                                                                                                                                121 AA
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HO P.L., SOARES M.B., YAMANE T., RAW I.;
J. TOXICOL. TOXIN. REV. 14:327-337(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUKARYOTA; METAZOA; CHORDATA; VERTEI
SCIUROGNATHI; MURIDAE; MURINAE; MUS
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[2]
SEQUENCE FROM N.A.
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                           STRAIN-VF5;
                                                                                             LIGASE.
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    SKARARO
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                                                                                                                                                                                                                                                                                                   HOMO SAPIENS (HUMAN).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                               TISSUE-BONE MARROW;
MEDLINE; 97191544.
MEDLINE; 97191544.
TANGASE T., SEKI N., ISHIKAWA K., OHIRA M., KAWARABAYASI Y., OHARA O.,
TANAKA A., KOTANI H., MIYAJIMA N., NOMURA N.;
"Prediction of the coding sequences of unidentified human genes. VI.
The coding sequences of 80 new genes (KIRAN201-KIRAN280) deduced by analysis of cDNA clones from cell line KG-1 and brain.";
DNA RES. 3:31-329 (1996).
EMBL; D86880; D1013905;
PFRM; PF00515; TPR; 1.
                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
             natriuretic peptide from the South American
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 98196666.

MEDLINE; 98196666.

GRASTERLAND T., YOUNG W.G., LENOX A.L.,
GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER
FELDMAN R.A., SHORT J.M., OLSON G.J., SNANSON R.V.;
The complete genome of the hyperthermophilic bacterium Aquifex
aeolicus.";
NATURE 392:353-358(1998).
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                                                                                                       Length 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 62, DB 4; Length 336;
Pred. No. 7.33e-01;
3; Mismatches 2; Indels
                                                                                                                             4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-NOY-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
UDP-N-ACETYLMURAMATE-ALANINE LIGASE.
                                                                                                                                                                                                                                 092623;
01-FEB-1997 (TREMBLREL. 02, CREATED)
01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                     Score 86; DB 13; I
Pred. No. 4.04e-06;
RAW I.;
"Cloning of an unusual natriuretic peptide from coral snake Micrurus corallinus.";
EURL J. BICCHEM. 250:144-149(1997).
EMBL; U77596; G1684874;
PROSITE; PSOU263: NATRIURETIC_PEPTIDE; 1,
PERM: PF00212; ANP: 1.
PEQUENCE 139 AA; 14881 MM; 05421ABB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 336 AA; 35417 MW; 62C3199B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BACTERIA; AQUIFICALES; AQUIFICACEAE; AQUIFEX
                                                                                                                             2; Mismatches
                                                                                                                                                                                                                      336 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  454 AA
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                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                MYELOBLAST KIAA0227 (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 45.3%;
Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                     Query Match 62.8%;
Best Local Similarity 64.7%;
Matches 11; Conservative
                                                                                                                                                   86 CFGQRIDRICNVSGMGC 102
                                                                                                                                                                 1 CFGGRMDRIGAQSGLGC 17
                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 GGRMERKGSAAG 123
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067373
067373;
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CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-36 FROM N.A.
RAMOS-MORALES F., ROMENO F., SCHWEIGHOFFER F., BISMUTH G., CAMONIS J.,
TORTOLERO M., FISCHER S.;
ONCOGENE 11:1665-1669(1995).
DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L., GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER R., FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.; SUBMITTED (JUL. 1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, AE000736; G2983764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                            Score 60; DB 2; Length 454;
Pred. No. 1.82e+00;
5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 60; DB 4; Length 539;
Pred. No. 1.82e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
ROMERO F.;
SUBMITTED (JAN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ROMERO F.;
SUBMITTED (MAR-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                                                                                                       SEQUENCE 454 AA; 50893 MW; 1207F9CE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                     539 AA
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                                                                                                                                                                                                                                                                                                                                                                   PRT;
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PFAM; PF00018; SH3; 2.
PFAM; PF00130; DAG_PE-bind; 1.
PFAM; PF00169; PH; 1.
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01,
08,
                                                                                                                                                            Query Match
Best Local Similarity 46.7%;
Matches 7; Conservative
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Best Local Similarity 46.7%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ULT 10
019208 PRELIMINARY;
019208;
01-NOV-1996 (TREMBLREL. 0:
01-NOV-1998 (TREMBLREL. 0:
01-NOV-1998 (TREMBLREL. 0:
COSMID FOBF8.
                                                                                                                                                                                                                                                                                                                                            1LT 9 PRELIMINARY;
015860 015860;
01-NOV-1996 (TREMBLREL. 0:
01-NOV-1998 (TREMBLREL. 0:
01-NOV-1998 (TREMBLREL. 0:
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                                                                                                                                                                                                                                              139 IGGRLKRLGTNAKLG 153
                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ::| |:| |:| |:
2 FGGRMDRIGAOSGLG 16
                                                                                                                                                                                                                                                                                 2 FGGRMDRIGAQSGLG 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOMO SAPIENS (HUMAN)
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NON_TER 539 :
SEQUENCE · 539 AA;
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RESULT

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STRAIN-PCC6803;
MEDLINE; 97061201.
KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
MIYAJIMA I., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S.,
SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
                                                                                                                                                                                                                                                                                MILSON R., BAYNES C., BERKS M.,
BONFIELD J., BURKOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURKON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
GRANDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
LIGHTNING J., LLOYD C., MCHURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
SWALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
HHIERRY-MIEG J., THOMAS.K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK E., WILKINSON-SPROAT J., WOHLDMAN P.;
1.2.2 M. of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                      CAENORHABDITIS ELEGANS.
EUKARYOTA: METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 59; DB 5; Length 352;
Pred. No. 2.84e+00;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYNECHOCYSTIS SP. (STRAIN PCC 6803).
BACTERIA; CYANOBACTERIA; CHROOCOCCALES; SYNECHOCYSTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TABATA S.;
SUBMITTED (JUN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BRISTOL N2;
WATERSTON R.;
SUBMITIED (JUN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U28991; G861369; -.
SEQUENCE 352 AA; 40771 MW; 31044A7A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBMITTED (JUN-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                         LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                                           CREATED)
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06,
06,
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01,
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Best Local Similarity 50.0%;
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12 12 PRELIMINARY; 019209; 019209; 01-NOV-1996 (TREMBLREL. 0 01-NOV-1996 (TREMBLREL. 0 01-NOV-1998 (TREMBLREL. 0 COSMID F08F8.
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01-FEB-1997 (TREMBLREL.
01-JAN-1999 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NATURE 368:32-38(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-BRISTOL N2; MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-PCC6803;
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P72780
P72780;
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                                                                               SEQUENCE FROM N.A.

C STRAIN-BRISTOL N2;

MEDLINE; 94150718.

MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

MILSON R., AINSCOUGH R., CONNELL M., COPSET T., COOPER J.,

CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

AGRONER A., GREEN P., HAWKINS T., HILLIER M., JOHNSTON L.,

LIGHTNING J., LLOYD C., MAWURRAY A., MORTIMORE B., O'CALLAGHAN M.,

PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERON J.,

MATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

12. Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDILINE: 97074647.

ZEKRI S., TORO N.:

Indentification and nucleotide sequence of Rhizoblum mellloti
Insertion sequence ISRM6, a small transposable element that belongs
to the IS3 family.";
GENE 175:4348(1995).

ERBNL: X95567; E221839; -
SEQUENCE 307 AA: 33688 MW; 8B9F5785 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                    EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      052960;
01-NOY-1996 (TREMBLREL. 01, CREATED)
01-NOY-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOY-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
01NKNOWN PRODUCT.
RHIZOBIUM PRELILOTI.
BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RHIZOBIACEAE GROUP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Pred. No. 2.84e+00;
.5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
WATERSTON R.;
WATERSTON R.;
EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U28991; G861368; -
SEQUENCE 281 AA; 32314 MW; A80C66BA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 59; DB 5; Le
Pred. No. 2.84e+00;
2; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     307 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RHIZOBIACEAE; SINORHIZOBIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         larity 41.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 43.1%;
Local Similarity 50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 CSGGRESRPASTASIGC 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFGGRMDRIGAOSGLGC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 CFGGRRARSASPIG 189
                                                                                                                                                                                                                                                                                                                                                                              NATURE 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFGGRMDRIGAQSG 14
        CAENORHABDITIS ELEGANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBMITTED (JUN-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 7; Conserv
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Query Match

Best Loca Matches

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STRAIN-GR4;

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US-09-027-777B-1.rspt

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Search completed: Wed Jun 16 13:16:30 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Gaps
              "Sequence analysis of the genome of the unicellular cyanobacterium Synchocystis sp. PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA RES. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSEUDOMONAS AERUGINOSA.
BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PSEUDOMONAS GROUP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular cloning, structure, and expression of mouse estrogen-responsive finger protein (efp): co-localization with estrogen receptor mRNA in target organs.";
J. Blod. CHEM. 270:24406-24413(1995).
-: SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 96210657.
OCHSNER U.A., VASIL M.L.;
"Gene repression by the ferric uptake regulator in Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 59; DB 11; Length 634; Pred. No. 2.84e+00; 5; Mismatches 2; Indels
                                                                                                                                                                                                              Score 59; DB 2; Length 394;
Pred. No. 2.84e+00;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIMO A., INOUE S., IKEDA K., NOJI S., MURAMATSU M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
ESTROGEN-RESPONSIVE FINGER PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AGG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
HYDROXAMATE-TYPE FERRISIDEROPHORE RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  634 AA; 71772 MW; 240021EF CRC32;
                                                                                                                                                                           394 AA; 41336 MW; 87507759 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                      634 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D63902; D1010590; -.
PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.
MGD; MGI:102749; ZFP147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1998 (TREMBLREL. 07, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE-UTERUS, OVARY, PLACENTA;
MEDLINE; 96025835.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00097; zf-C3HC4; 1.
ZINC-FINGER.
                                                                                                                                                                                                              Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 50.0%;
Matches 8; Conservative
                                                                                      EMB: D90900; D1017528; --
PFAM: PF00089; LTypsin; 1
PFAM: PF00595; PDZ; 1.
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| CFGGRMDRIGAQSGLG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                              353 GARLQRIVEQAGL 365
                                                                                                                                                                                                                                                                                                                     1:|::|| |:||
3 GGRMDRIGAQSGL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUS MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                      PROTEASE.
SEQUENCE
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061510
061510;
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068595
068595;
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Pred. No. 2.84e+00;
6; Mismatches 1; Indels
aeruginosa: cycle selection of iron-regulated genes.";
PROC. NATL. ACAD. SCI. U.S.A. 93:4409-4414(1996).
                                                                                                                       OCHSNER U.A., VASIL A.I., JOHNSON Z., VASIL M.L.;
SUBMITTED (MAR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, AF051691; G2981048; -
SEQUENCE 802 AA: 88271 MW; 02BD9E37 CRC32;
                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 50.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      2 FGGRMDRIGAQSGL 15
                                                                                                                                                                                                                                                                                                                                                            44 LAGTLNRIAAQAGL 57
                                                                          SEQUENCE FROM N.A.
                                                                                                     STRAIN-PAO1;
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117 118 118 118 119 118 119 119 119 119 119	RESULT 1 ID P50493 st	P50493; 18-MAR- Cardiod Cardiod W085028 W085028 04-JUL- 21-DEC- 24-DEC- (ORGA-)	WPI New Sec Cla	•	CC the treat control of the tr
Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Ediburgh, U.K. Distribution rights by Oxford Molecular Ltd MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Run on: Wed Jun 16 13:18:27 1999; MasPar time 3.46 Seconds 92.241 Million cell updates/sec Title: Description: (1-15) from US09027777B.pep Perfect Score: 101 Sequence: LRALLTAPRSLERSS 15	Searched: 170751 seqs, 21266608 residues Post-processing: Minimum Match O% Listing first 45 summaries	art2 5:pa 0:pa 5:pa 5:pa	Statistics: Mean 19.236; Variance 74.819; scale 0.257 Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES Result Query No. Score Match Length DB ID Description Pred. No.	1 101 100.0 88 3 P50493 Cardiodilatine peptid 1.82e-02 101 100.0 125 1 P82656 Vasodilatory peptide. 1.82e-02 3 100.0 126 3 P50037 Sequence of human gam 1.82e-02 4 101 100.0 126 27 W34533 Human atrial na 1.82e-02 Human gamma atrial na 1.82e-02 101 100.0 126 4 P51240 Sequence of pro-atria 1.82e-02 Human pre-proANVP #2. 1.82e-02 Human pre-proANVP #2. 1.82e-02 101 100.0 136 7 R36935 Human pre-proANVP #2. 1.82e-02 101 100.0 150 4 P51241 Sequence of pre-pro-a 1.82e-02 10 100.0 150 4 P51241 Sequence of pre-pro-a 1.82e-02 11 101 100.0 151 3 P50036 Sequence of pre-pro-a 1.82e-02 12 101 100.0 151 3 P50036 Sequence of the precu 1.82e-02 13 101 100.0 151 3 P50036 Sequence of the precu 1.82e-02 13 101 100.0 151 3 P50036 Sequence of the precu 1.82e-02 14 101 100.0 151 3 P50036 Rat atrial natriureti 6.74e-02 15 94.1 48 3 P50115 Rat atrial natriureti 6.74e-02 16 95 94.1 62 3 P60165 Rat recombinant pro-c 6.74e-02

Sequence of peptide(s 6.74e-02 Sequence of atrial na 6.74e-02 Sequence of polypepti 6.74e-02 Atrial natriuretic fa 6.74e-02 Sequence of cardionat 6.74e-02 Sequence of pro-atria 6.74e-02 Sequence of pre-pro-a 6.74e-02 Sequence of the exten 2.54e-00 Sequence of the exten 2.54e-00 Sequence of atrial na 2.99e-01 Atrial natriuretic fa 8.83e-03 Sequence of atrial na 2.99e-01 Atrial natriuretic fa 2.99e-01 Atrial natriuretic fa 2.99e-01 Atrial natriuretic fa 2.99e-01 Sequence of peptide h 2.99e-01	RESULT 1 ID P50493 standard; protein; 88 AA. AC P50493. AC S16493 standard; protein; 88 AA. BC P50493. BC T 18-MAR-1992 (first entry) BC Cardiodilatine peptide hormone variant. KW Cardiodilatine; peptide; hormone; hypotensive; ss. PN W08502850-A. DO 4-JUL-1985. PP C-1984: D00279. PR 24-DEC-1984: D00279. PR 54-DEC-1984: D00279. PR 54-DEC-1984: D00279. PR 6fects on heart muscle ionotropy, smooth muscle, and sweat secretion and an isoelectric point of 6-6.5. This peptide CC This variant of the peptide described in P50491 has a mol.wt. CC This variant of the peptide described in P50491 has a mol.wt. CC This variant of the peptide described in P50491 has a mol.wt. CC This variant of the peptide described in P50491 has a mol.wt. CC This variant of the peptide described in pcoups and contain the largenesis and therapy of hypertension. It can also be used for the treatment of post-operative cardiovascular disorders, skin cc the treatment of post-operative cardiovascular disorders, skin cc transcribed in P50491-2. Sequence 88 AA;	101; DB 3; Length 88; No. 1.82e-02; ismatches 0; Indels 0; Gaps
P51102 P50107 P50107 P501055 P50107 P501033 P51238 P51238 P51238 P51242 P51242 P600325 P71677 P61086 P61055 P7165	ALIGNMENT 8 AA. 1 Inatine - 1 otropy, s 1 man 1 describe 2 point o 2 point o 2 point o 3 perween 1 p	Score Pred. 0; M
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RESULT 2 ID P82656 standard; protein; 125 AA.

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hypertension; cirrhosis; nephrosis; heart disease
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09-MAR-1995; US-401246.
29-SEP-1987; US-102477.
01-MAY-1990; US-517552
14-NOV-1991; US-799211.
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                                 10-JAN-1988
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                                                                                                                   Biologically prepared peptide -
has vein relaxation activity.

Claim 1; page 1; 13pp; Japanese
This sequence as isolated from human heart. Sequences complementary
to the DNA encoding MDRIG of cardionatrin were isolated using
a mixture of oligonucleotide probes. Two plasmids, phavD and phMANF,
identified by this screening process, were then used to transform
Sequence 125 AA;
                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NP-SDB; N50055.

New DNA sequences from human atrium cordis - coding for new diuretic polypeptide or precursor cpds.

Claim 26; Page 37: 53pp; English.

The precursor of human gamma-ANP and its 26Asn-151Tyr fragmentare claimed (P50036, P50037), as are the DNA SQs encoding them (N50020, N30055). The 26Asn-151Tyr fragment has a diuretic action so is useful as a hypotensive/antihypertensive agent. The usual dose is
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Sequence of human gamma-atrium natriuretic polypeptide (ANP).
Natriuretic; diuretc; hypotensive; antihypertensive.
EP-164273-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 100.0%; Score 101; DB 3; Length 126; Best Local Similarity 100.0%; Pred. No. 1.82e-02; Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                        Length 125
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R00582 standard; protein; 126 AA.
R00582.
05-JUN-1989 (first entry)
Human gamma atrial natriuretic polypeptide (gamma-hANP).
Gamma atrial natriuretic polypeptide; ANP; natriuretic;
                                                                                                                                                                                                                                                              0; Indels
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08-JUN-1984; 116605.
08-JUN-1984; JP-116606.
08-JUN-1984; JP-116605.
(SUNR) SUNYORY LTD.
Matsuo H, Kangawa K, Hayashi Y, Oikawa S, Oshima
                                                                                                                                                                                                                                        Score 101; DB 1;
Pred. No. 1.82e-02;
                                                                                                                                                                                                                                                              0; Mismatches
                      Vasodilatory peptide.
vasodilatory peptide; cardionatrin.
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P50037 standard; Protein; 126 AA.
P50037;
                                                                                              (MITU) Mitsubishi Chem Ind KK. WPI; 88-170991/25.
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Best Local Similarity 100.0%;
Matches 15; Conservative
              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LRALLTAPRSLRRSS 15
                                                                                       18-SEP-1986; JP-220835.
                                                                 12-MAY-1988.
18-SEP-1986; 220835.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 85-312162/50.
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            16-NOV-1990
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peptide fragment of hypertension and related disorders - with synthetic peptide fragment of atrial natriuretic factor pro:hormone Disclosure; Column 4: 19pp; English.

Disclosure; Column 4: 19pp; English.

This sequence represents the human atrial natriuretic factor prohormone (proANF). Fragments of this sequence (see W34521-W34523) can be used in the method of the invention. The method is for treating hypertension, congestive heart failure, pulmonary odedma, toxaemia of pregnancy, nephrotic syndrome, acute and chronic renal failure or hepatic cirrhosis with or without ascites comprises administering a synthetic peptide with or without ascites comprises administering a synthetic peptide with or without ascites comprises administering a synthetic peptide constitution and proANF(1-30) and proANF(1-30) and also be used in a method for treating hyperkalaemia associated with acidosis, digitalis overdose, succinylcholine, insulin deficiency, acute or chronic renal failure, duretic, natriuretic and/or kaliuretic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of pregnancy;
hyperkalaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                   Monoclonal antibodies recognising gamma-atrial natriuretic used for diagnosis of diseases eg kidney and heart disease. Disclosurer: Fig. 1: 10pp; English. Gamma-hANP of which the N-terminal 25 AAs are recognisy monoclonal antibodies of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-MAR-1998 (first entry)
Human atrial natriuretic factor prohormone.
Human atrial natriuretic factor prohormone, therapy; hypertension; congestive heart failure; pulmonary oedems; toxaemia of pregnancy; nephrotic syndrome; renal failure; hepatic cirrhosis; hyperkalaemia acidosis; digitalis overdose; insulin deficiency; Addison's disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 101; DB 2; Length 126;
Pred. No. 1.82e-02;
0; Mismatches 0; Indels
30-JUN-1989; 306669.
04-JUL-1988; JP-166641.
(SIIO) Shionogi Seiyaku Kabushiki.
Imura H, Nakao K;
WPI; 90-009970/02.
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W34533 standard; Protein; 126 AA.
W34533;
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Best Local Similarity 100.0%;
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Best Local Similarity 100.0%;
Matches 15; Conservative
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Gaps

US-09-027-777B-2.rag

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(MATS/) Matsuo T. (MATS/) Matsuo M
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Pred. No. 1.82e-02;
0; Mismatches 0; Indels
                         Length 136;
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Johnson LK, Atlas SA, Mccarthy BJ, Laragh JH, Lewickl JA,
WPI, 85-289554/46.
WP FSDB, N50655, N50763.
New atrial polypeptide cpds. - useful as natriuretics,
diuretics, vasodilators and modulators of the
renin anglotensin aldosterone system
Sequence of pre-pro-atrial natriuretic/vasodilator polypeptide (ANVP).
Natruiretic; duiretic; vasodilator; venin-angiotensin-aldosterone-system.
                                                                                                                                                                                                                                                                                                                                                                            Sequence of pre-human atrial natriuretic peptide.
Human-chANP; diuretic; antihypertensivity; ss.
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P51241 standard; peptide; 150 AA.
P51241;
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Best Local Similarity 100.0%;
Matches 15; Conservative
                            Query Match
Best Local Similarity 100.0%;
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                                                                                    15; Conservative
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                                                                                                                                   100 lralltaprslrrss 114
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14-JUL-1988; 173739.
14-JUL-1988; JP-173739.
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01-JUN-1984; US-616488.
20-JUN-1984; US-622639.
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150 AA;
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This sequence is encoded by the human pre-pro atrial natriuretic/
vascallator peptide (ANP) cDNA. Fragments of this protein and the
corresponding sequence in rat (see also R36936), may be used for
regulation of fluid volume and blood pressure in host organisms.
The ANVP fragments may be produced by solid-phase techniques. See
also R36937-78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vasodilator polypeptide (ANVP), pro-ANVP or pre-pro-ANVP, or their fragments. The encoding DNA sequence is also claimed. The claimed polypeptides are natriuretics, diuretics, vasodilators and modulators of the renin-angiotensin-aldosterone system. Dose is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             renin-angiotensin-aldosterone system
Claim 8: Page 116: 144pp; English.
The inventors claim a polypeptide comprising atrial natriuretic/
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                                                     03-AUG-1992 (first entry)
Sequence of pro-atrial natriuretic/vasodilator polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Johnson LK, Atlas SA, Mccarthy BJ, Laragh JH, Lewicki JA, WPI: 85-289654746.
New atrial poly:peptide cpds. - useful as natriuretics, diuretics, vasodilators and modulators of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 101; DB 4; Length 126
Pred. No. 1.82e-02;
0; Mismatches 0; Indels
                                                                                                                                 Natruiretic; duiretic; vasodilator;
venin-angiotensin-aldosterone-system.
                                                                                                                                                                                                                       Location/Qualifiers
P51240 standard; peptide; 126 AA.
P51240;
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105..121
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Local Similarity 100.0%;
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09-APR-1984; US-602117.
00-JUN-1984; US-616488.
08-MAY-1985; US-766030.
05-JUN-1986; US-766030.
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20-JUN-1984; US-622639
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Sequence 126 AA;
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modified_site
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Matsuo H, Kangawa K, Hayashi Y, Oikawa S, Oshima T, Tanaka S, Wakazato H, Tawaragi Y; Tanaka S, Wakazato H, Tawaragi Y; Tanaka S, Wakazato H, Tawaragi Y; MwP1: 85-312162/50.

New DNA sequences from human atrium cordis - coding for new odiuretic polypeptide or precursor cpds.

Claim 25; Fig 5; 53pp; English.

The precursor of human gamma-ANP and its 26Asn-151Tyr fragmentare claimed (P50036, P50037), as are the DNA SQs encoding them (N50020, M50055).

W50055). The 26Asn-151Tyr fragment has a diuretic action so is useful as a hypotensive/antihypertensive agent. The usual dose is
  Genetic analysis diagnostic for hypertension - by detecting polymorphous of the renin, kallikrein or ANF gene regions bisclosure; Fig 2: 51pp; English.

The patent application is for a method used for determn. of a genetic fingerprint of a subject which allows early diagnosis of individuals at risk of hypertension and permits early therapeutic measures to prevent the fatal symptomology of the disease. The section of the genome which is fingerprinted or otherwise subject study using the results is dependent on the nature of the probestudy probes useful in the present invention are selected from the renin, kallikrein, or ANF gene (see FT).
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Cardiodilatin; plasmid pHANF48; muscle relaxant; antihypertensive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P50036;
03-SEP-1991 (first entry)
Sequence of the precursor of human gamma-atrium natriuretic
polypeptide (ANP).
Natriuretic; diuretc; hypotensive; antihypertensive.
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Pred. No. 1.82e-02;
0; Mismatches 0; Indels
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Pred. No. 1.82e-02;
0; Mismatches 0; Indels
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P50036 standard; Protein; 151 AA.
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P50050 standard; protein; 151
P50050;
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Best Local Similarity 100.0%;
Matches 15; Conservative
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Best Local Similarity 100.0%;
Matches 15; Conservative
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08-JUN-1984; JP-116606.
08-JUN-1984; JP-116605.
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21-JUN-1984; JP-1283
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12-OCT-1984; JP-21389
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EP-159943-A.
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EP-164273-A.
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Claim 7; Page 115; 144pp; English.
The inventors claim a polypeptide comprising atrial natriuretic/
vasodilator polypeptide (ANVP), pro-ANVP or pre-pro-ANVP, or their
fragments. The encoding DNA sequence is also claimed. The claimed
polypeptides are natriuretics, diunetics, vasodilators and
modulators of the renin-angiotensin-aldosterone system. Dose is
                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-APR-1991 (first entry)
Sequence encoded by human atrial natriuretic peptide factor (ANF)
                                                                                                                                                                                                                                                                                                                                                         03-AUG-1992 (first entry)
Sequence of pre-pro-atrial natriuretic/vasodilator polypeptide
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07-NOV-1985.
19-APR-1985.
19-APR-1984; US-602117.
01-JUN-1984; US-61248.
20-JUN-1984; US-612648.
(BIOT-) BIOTECHNOL RES PART.
Johnson LK, Allas SA, Mccarthy BJ, Laragh JH, Lewicki JA; WPI; 85-289654/46.
                          Length 150;
                                                                               Indels
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the
Score 101; DB 4; Ler
Pred. No. 1.82e-02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jone fingerprinting; probe; hypertension. Homo sapiens. WO8702709-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Natruíretic; duiretic; vasodilator; venin-angiotensin-aldosterone-system.
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                                                                                                                                                                                                                                                                             .r 10
P51239 standard; peptide; 150 AA.
P51239;
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N-PSDB; N70974.
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24-OCT-1985; US-790813.
12-NOV-1985; US-796904.
09-JAN-1986; US-8173.
11-UUN-1986; US-873199.
(BIOT-) BIOTECHN RES PARTN.
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Best Local Similarity 100.0%;
Matches 15; Conservative
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Best Local Similarity 100.0%;
Matches 15; Conservative
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Sequence 150 AA;
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RESULT 10 PV 11 PV 12 PV 12 PV 14 PV 14 PV 15 PV 16 PV

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                                                                           corresp. DNA sequences, useful as antihypertensive agents.
Disclosure; Fig. 13: 45pp; English.
The DNA encoding the cardiodilatin is carried on plasmid pHANF48.
Cardiodilatin is a muscle relaxant, so is useful as an antihypertensive agent. The DNA is obtd. from RNA isolated from the human heart.
Sequence 151 AA;
                                                                Expression vector contg. gene for cardionatrin or cardiodilatin - and
                                                                                                                                                                                                               Gaps
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This sequence is encoded by the human pre-pro atrial natriuretic/vasodilator peptide (ANVP) DNA. Fragments of this protein and the
                                                                                                                                                                                                                                                                                                                                                     14-SEP-1993 (first entry)
Human pre-proANVP #1.
Human: pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
regulation; fluid volume; blood pressure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   corresponding sequence in rat (see also N36936), may be used for regulation of fluid volume and blood pressure in host organisms. The ANVP fragments may be produced by solid-phase techniques. Sealso R36937-78.
                                                                                                                                                                                                             ö
(MITU) Mitsubishi Chemical Industries Ltd.
Nakanishi S, Teranishi Y, Nagahari K, Shibui T, Takamatsu K;
WPI; 85-271495/44.
N-PSDB; N50069.
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Pred. No. 1.82e-02;
0; Mismatches 0; Indels
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C P50115;
T 22-OCT-1991 (first entry)
E Rat atrial natriuretic factor-beta.
A Atrial natriuretic factor; diuretic; hypotensive.
Key
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/note= "Mature protein"
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R36934 standard; Protein; 151 AA.
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Best Local Similarity 100.0%;
Matches 15; Conservative
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01-JUN-1984; US-616488
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05-JUN-1986; US-870795
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PN EF153865-A.
PD 04-SEP-1985.
PP 153865-A.
PP 04-SEP-1985.
PF 28-FEB-1985.
PR 02-MAR-1984.
PP 02-MAR-1984.
PP 02-MAR-1984.
PP 02-MAR-1984.
PP 02-MAR-1984.
PP 02-MAR-1984.
PP 03-MATCH
PT MATSON H.
PT ATTIUM COTCHS.
PS Claim 1: Page 17: 23pp; English.
CC The rat atrial natriuretic factor-beta has diuretic, natriuretic and cC hypotensive or hypertensive activity.
CC The rat arrial natriuretic factor-beta has diuretic, natriuretic and cC hypotensive or hypertensive activity.

Query Match
Sequence 48 AA;

Query Match
Best Local Similarity 86.7%; Pred. No. 6.74e-02;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Db 12 IrallagprsIrrss 26
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Oy 1 LRALITAPRSIRRSS 15
Search completed: Wed Jun 16 13:18:45 1999
Job time : 18 secs.
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US-09-027-777B-2.rai

		2. Applicatio 7.9 8. Applicatio 1.11 8. Applicatio 1.11 24. Applicati 1.4 24. Applicati 1.4 25. Applicati 1.4 26. S460961 1.4 27. Applicatio 1.7 28. Applicatio 1.7 29. Applicatio 1.7 29. Applicatio 1.7 20. Applicatio 1.7 20. Applicatio 1.7 21. Applicatio 1.7 22. Applicatio 1.7 23. Applicatio 1.7 24. Applicatio 1.7 25. Applicatio 1.7
Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd MPsrch_pp protein - protein database search, using Smith-Waterman algorithm		53 52.5 824 1 US-08-221- Sequence 3, Applicatio 1 53 52.5 857 3 PCT-US96-1 Sequence 2, Applicatio 1 53 52.5 857 2 US-08-59- Sequence 2, Applicatio 1 53 52.5 947 3 PCT-US95-0 Sequence 19, Applicati 1 53 52.5 3077 4 5223423-2 Patent No. 5223423.
Run on: Wed Jun 16 13:21:01 1999; MasPar time 1.40 Seconds 108.644 Million cell updates/sec Tabular output not generated.	· ·	52 51.5 1810 3 PCT-US95-1 Sequence 4, Applicatio 2.0 51 50.5 1162 2 US-08-663- Sequence 15, Applicati 2.0 51 50.5 2910 2 US-08-461- Sequence 183, Applicat 2.0 50.5 20.5 20.5 20.5 20.5 20.5 20.5
Title: >US-09-027-777B-2 Description: (1-15) from US09027777B.pep Perfect Score: 101 Sequence: 1 LRALLTAPRSLERSS 15	RESULT	ALIGNMENTS 1
Scoring table: PAM 150 Gap 15	YX TD	US-08-737-927-2 STANDARD; PRT; 15 AA. xxxxxx
Searched: 106580 segs, 10152877 residues	XX	
Post-processing: Minimum Match 0% Listing first 45 summaries	X D X	
Database: a-issued 1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1	888	pplicatic 67239 RMATION:
Statistics: Mean 17.828; Variance 71.575; scale 0.249	888	APPLICANT: IMMER, Hansuel1 APPLICANT: FORSSMANN, Wolf-Georg
Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	88888	CANT: CANT: OF INV
SUMMARIES	888	TITLE OF INVESTION: CARDIODILATIN FRAGMENTS NUMBER OF SEQUENCES: 5 CORRESPONDENCE ADDRESS:
Result Ouery No. Score Match Length DB ID Description Pred. No.	888	ADDRESSEE: Nikaido, Marmelstein, Murray 6 Oram STREET: 655 Fifteenth Street N.W. Suite 330
101 100.0 15 2 US-08-737- Sequence 2, Applicatio 8.81 101 100.0 136 4 5212286-4 Patent No. 5212286. 8.81 101 100.0 151 4 5212286-2 Patent No. 5212286. 8.81	888	STATE: D.C. COUNTRY: U.S.A. ZIP: 2005-5701
95 94.1 152 4 5212286-6 Patent No. 5212286. 79 78.2 144 4 5202239-3 Patent No. 5202239. 79 78.2 144 4 5202239-1 Patent No. 5202239.	888	COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC commatible
64 63.4 16 4 5449751-4 Patent No. 5449751. 2.01	888	OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30
64 63.4 32 4 3449/31.3 Patent No. 3449/31. 64 63.4 32 3 PCT-US94-1 Sequence 2, Applicatio 64 63.4 32 0S-08-470- Sequence 15, Applicatio	888	CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/737,927 FILING DATE:
64 63.4 32 2 US-08-470- Sequence 18, Applicati 2.01 64 63.4 32 2 US-08-737- Sequence 4, Applicatio 2.01	888	CLASSIFICATION: 424 PRIOR APPLICATION DATA:
ov 05:4 32 3 PCT-US94-1 Sequence 5, Applicatio 2.01 64 63.4 32 2 US-08-470- Sequence 5, Applicatio 2.01 64 63.4 32 2 US-08-470- Sequence 5, Applicatio 2.01	388	AFFLICKION NUMBER: WO 95/33/09 FILING DATE: 14-DEC-1995 ATTORNEY, AGENT INFORMATION:
64 63.4 32 1 US-08-451- Sequence 2, Applicatio 64 63.4 32 1 US-08-451- Sequence 15, Applicatio 64 63.4 32 1 US-08-451- Sequence 5, Applicatio	ខ្លួន 	NAME: 'Kitts, Monica C. - REGISTPATION NUMBER: 36,105 - REFERENCE/DOCKET NUMBER: 91614-6052
20 1 US-08-401- Sequence 3, Applicatio 2.45 642 1 US-08-414- Sequence 25, Applicati 4.42 528 4 547599-2 Patent No. 5475095. 5.37 529 4 5217865-2 Patent No. 5217865. 5.37	8888	TELECOMMUNICATION INFORMATION: TELEPHÓNE: (202)638-5000 TELEFAX: (202)638-4810 INFORMATION FOR SEQ ID NO: 2:

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Gaps
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Pred. No. 8.81e-03;
0; Mismatches 0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/870,795
FILING DATE: 05-JUN-1986
APPLICATION DATA:
APPLICATION NUMBER: 766,030
FILING DATE: 08-MAY-1985
APPLICATION NUMBER: 602,117
FILING DATE: 09-APR-1984
APPLICATION NUMBER: 616,488
FILING DATE: 01-JUN-1984
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NUMBER OF SEQUENCES: 16
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/564,259
FILING DATE: 07-AUG-1990
                                                                                              164 AA; 17827 MW; 143008 CN;
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FILING DATE: 08-MAY-1985
APPLICATION NUMEER: 602,117
FILING DATE: 09-APR-1984
FILING DATE: 01-JUN-1984
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Best Local Similarity 86.7%;
Matches 13; Conservature
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Best Local Similarity 100.0%;
Matches 15; Conservative
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| LRALLTAPRSLRRSS 15
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LENGTH: 151
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Pred. No. 8.81e-03;
0; Mismatches 0; Indels
                                                                                                            Length 15;
                                                                                                                                      0; Indels
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TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
PEPTIDE COMPUNDS
NUMBER OF SEQUENCES: 68
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/870,795
FILING DATE: 05-UN-1986
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M. TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR PEPTIDE COMPUNDS
                                                                                                         Score 101; DB 2;
Pred. No. 8.81e-03;
0; Mismatches 0
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/870,795
FILING DATE: 05-JUN-1986
APPLICATION NUMBER: 766,030
FILING DATE: 08-MAY-1985
APPLICATION NUMBER: 602,117
FILING DATE: 09-APR-1984
APPLICATION NUMBER: 616,488
FILING DATE: 01-JUN-1984
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                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE 15 AA; 1697 MW; 1159 CN;
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                  15 amino acids
  SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.0%;
Matches 15; Conservative
                                                                                                         Query Match
Best Local Similarity 100.0%;
Matches 15; Conservative
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ID 5212286-4
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C GERHARD; HERBST, FRANZ
C GERHARD; HERBST, FRANZ
C TITLE OF INVENTION: CARDIODILATIN FRAGMENT, PROCESS FOR
TITLE OF INVENTIONS ENDEROFF
C NUMBER OF SEQUENCES: 4
CURRENT APPLICATION NUMBER: US/08/185,240
FILING DATE: 14-JAN-1994
C FILING DATE: 16-DEC-1992
C FILING DATE: 16-DEC-1992
C FILING DATE: 18-NOV-1991
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TITLE OF INVENTION: CARDIODILATIN FRAGMENT, PROCESS FOR PREPARING SAME AND USE THEREOF
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                                 Score 64; DB 4; Lo
Pred. No. 2.01e+01;
0; Mismatches 0
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Pred. No. 2.01e+01;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,240
FILING DATE: 24-JAN-1994
PRIOR AFPLICATION DATA:
APPLICATION NUMBER: 994,084
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: 795,248
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17 AA; 1892 MW; 1532 CN;
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APPLICATION NUMBER: 100,144
FILING DATE: 28-AUG-1987
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APPLICATION NUMBER: 401,401
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Best Local Similarity 100.0%;
Matches 10; Conservative
                                   Query Match 63.4%;
Best Local Similarity 100.0%;
Matches 10; Conservative
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APPLICANT: TARNOWSKI, JOSEPH S.;HILLIKER, SANDRA; WILLETT
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TITLE OF INVENTION: CARDIODILATIN FRAGMENT, PROCESS FOR PREPARING SAME AND USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 79; DB 4; Length 144; Pred. No. 9.45e-01; 1; Mismatches 0; Indels
                                                                       Length 144;
                                                                       Score 79; DB 4; Length 144; Pred. No. 9.45e-01; 1; Mismatches 0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,240
FILING DATE: 24-JAN-1994
PRIOR APPLICATION DATE: 994,084
FILING DATE: 16-DEC-1992
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NUMBER OF SEQUENCES: 16
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/564,259
FILING DATE: 07-AUG-1990
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ICE ' 156 AA; 17116 MW; 129679 CN;
                                 156 AA; 17115 MW; 129665 CN;
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FILING DATE: 01-SEP-1989
APPLICATION NUMBER: 100,144
FILING DATE: 28-AUG-1987
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Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                     Query Match

Best Local Similarity 91.7%;
Matches 11; Conservative
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APPLICATION NUMBER
FILING DATE: 18-NO
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           LENGTH: 144
SEQUENCE 156 AB.
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LENGTH: 16
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ID 5202239-1
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Gaps

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APPLICANT: Oare, David
APPLICANT: McDowell, Robert S.
APPLICANT: Burnier, John
TITLE OF INVENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC PEPTIDES
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
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                                        Indels
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ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
medium TYPE: 0.5 inch, 1.45 mb floppy disk
computeR: IBM PC compatible
compatible
compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 64; DB 2; Len
Pred. No. 2.01e+01;
0; Mismatches 0;
                                                                                                                                                                                                                                                                        32 AA.
         Pred. No. 2.01e+01;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: WinParin (Genericch)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,846A
FILING DATE: 06-Jun-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P0844P2C1
                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 06-Jun-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
FILING DATE: 11-APR-1995
FILING DATE: 11-APR-1995
PRIOR APPLICATION NUMBER: 08/36252
APPLICATION NUMBER: 08/36252
FILING DATE: 06-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/362594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15, Application US/08470846A
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15, Application US/08470846A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/152994 FILING DATE: 12-NOV-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Genentech, Inc.
APPLICANT: Lowe, David G.
APPLICANT: Cunningham, Brian C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOGY: Linear
32 AA; 3564 MW; 4811 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: PARTICULE TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Kubinec, Jeffrey REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 63.4%;
Best Local Similarity 100.0%;
Matches 10; Conservative
   Best Local Similarity 100.0%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 5846932
GENERAL INFORMATION:
                                                                                            1 TAPRSLRRSS 10
                                                                                                                                 1 TAPRSLRRSS 10
                                                                                                                                                                                                                                             RESULT 11
ID US-08-470-846A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                         Gaps
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APPLICANT: Cundingham, Brian C.
APPLICANT: Cundingham, Brian C.
APPLICANT: Oxoco David
APPLICANT: McDowell, Robert S.
APPLICANT: Burnier, John
TITLE OF INVENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC
TITLE OF INVENTION: APPLICES
NUMBER OF SEQUENCES: 47
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                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                        Score 64; DB 4; Length 32; Pred. No. 2.01è+01;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: C. ....
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
MEDIUM TYPE: P. Compatible
COUNTRER: IBM PC COMPATIBLE
COUNTRER: CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/12591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application PC/TUS9412591
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.4%; Score 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application PC/TUS9412591
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FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                             SEQ ID NO:3:
LENGTH: 32
SEQUENCE 35 AA: 3838 MW; 6483 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 AA; 3508 MW; 4652 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32,637
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REGIESTRATION NUMBER: 32,637
REFERENCE/DOCKET NUMBER: 84
TELECOMMUNICATION INFORMATION
FILING DATE: 18-NOV-1991
APPLICATION NUMBER: 401,401
FILING DATE: 01-SEP-1989
APPLICATION NUMBER: 100,144
FILING DATE: 28-AUG-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                     Query Match 63.4%;
Best Local Similarity 100.0%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                          1 TAPRSLRRSS 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ULT 10
PCT-US94-12591-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Gaps

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Sequence 4, Application US/08737927

Patent No. 5767239

GENERAL INFORMATION:
APPLICANT: INMER, Hansueli
APPLICANT: FORSSMANN, Wolf-Georg
APPLICANT: AND HIGHLY PURIS TITLE OF INVENTION: CARDIODILATIN FRAGMENTS, AND HIGHLY PURIS NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
ZIP: 2005-5701
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURREDY APPLICATION DATA:
APPLICATION NUMBER: US/08/737,927
                                                                                                                                                                                                                                                                                                                                                                                                       E: Nikaido, Marmelstein, Murray & Oram 655 Fifteenth Street N.W. Suite 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 AA.
                   32 AA.
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Pred. No. 2.01e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: P1614-6052 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: W0 95/33769
FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kitts, Monica C.
REGISTRATION NUMBER: 36,105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15, Application PC/TUS9412591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLÓGY: linear
MOLECULÉ TYPE: peptide
HENCE 32 AA; 3508 MW; 4652 CN;
                                                                                                                                   Sequence 4, Application US/08737927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (202)638-4810 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS:
                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 63.4%;
Best Local Similarity 100.0%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TAPRSLRRSS 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LT 14
PCT-US94-12591-15
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 JT 13
US-08-737-927-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
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                                                           XXXXXX
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                                                                                                                                                                                                                                                                                         APPLICANT: Generitech, Inc.
APPLICANT: Lowe, David G.
APPLICANT: Cunningham, Brian C.
APPLICANT: Oare, David
APPLICANT: Oare, David
APPLICANT: McDowell, Robert S.
APPLICANT: Burnier, John
TITLE OF INVENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC PEPTIDES
CORRESPONDENCE: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
NEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,846A
FILING DATE: 06-Jun-1995
CLASSIFICATION: 514
PRIOR APPLICATION UNBER: 08/419877
FILING DATE: 11-APR-1995
PRIOR APPLICATION NUMBER: 08/419877
FILING DATE: 11-APR-1995
FILING DATE: 06-JAN-1995
FILING DATE: 06-JAN-1995
FRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36.775
REFRENCE/COCKET NUMBER: P0844P2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-828
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 64; E
Pred. No. 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: Callifornia
                                                                                                                                                                                                              Patent No. 5846932
GENERAL INFORMATION:
APPLICANT: General Applicants
                                                                                                                                                                                                            Sequence 18, Application US/08470846A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/152994
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOGY: Linear
32 AA; 3508 MW; 4652 CN;
                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
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Best Local Similarity 100.0%;
Matches 10; Conservative
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6 TAPRSLRRSS 15
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US-09-027-777B-2.rai

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ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Pred. No. 2.01e+01;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                        SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/12591
FILING DATE:
                                                    ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: 08/152994
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Daryl B.
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32 AA; 3589 MW; 4484 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 910/371.7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 32 amino acids
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Best Local Similarity 100.0%;
Matches 10; Conservative
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                                                                                   APPLICANT: Lowe, David
APPLICANT: Cundingham, Brian C.
APPLICANT: Cundingham, Brian C.
APPLICANT: Mobowell, Robert S.
APPLICANT: Burnier, John
TITLE OF INVENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC
TITLE OF INVENTION: PEPTIDES
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
21P: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/12591
Sequence 15, Application PC/TUS9412591 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application PC/TUS9412591 GENERAL INFORMATION:
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Lowe, David
Cunningham, Brian C.
Oare, David
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/152994
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 15:
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 63.4%;
Best Local Similarity 100.0%;
Matches 10; Conservative
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APPLICANT:
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TELEX: 9
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed Jun 16 13:19:02 1999; MasPar time 3.25 Seconds 185.026 Million cell updates/sec Run on:

Tabular output not generated.

(1-15) from USO9027777B.pep 101 >US-09-027-777B-2 Description: Perfect Score: Sequence:

1 LRALLTAPRSLRRSS 15 Scoring table:

122810 segs, 40068593 residues PAM 150 Gap 15 Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Mean 27.259; Variance 42.565; scale 0.640 pir60 1:pirl 2:pir2 3:pir3 4:pir4 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	% Query Match Length DB	DB	Ω	Description	Pred. No.
: -	101	100.0	151	: -	AWHU	natriuretic peptide A	1.10e-07
~	101	100.0	152	-	AWBO	atrial natriuretic pe	1.10e-07
٣	101	100.0	153	٦	AWRB	atrial natriuretic pe	1.10e-07
₹.	96	97.0	149	-	AWDG	atrial natriuretic pe	4.64e-07
S	86	97.0	150	٦	S13107	_	. 4.64e-07
ø	86	97.0	153	~	S14873	atrial natriuretic pe	4.64e-07
7	95	94.1	128	~	S14872	atrial natriuretic pe	1.92e-06
œ	95	94.1	152	П	AWRT	atrial natriuretic fa	1.92e-06
0	95	94.1	152	Н	AWMS	atrial natriuretic pe	1.92e-06
10	88	87.1	145	~	300947	atrial natriuretic pe	4.96e-05
1	99	65.3	758	7	551748	lethal(2)denticleless	6.56e-01
12	65	64.4	196	~	E69100	hypothetical protein	9.77e-01
13	61	60.4	215	7	G70575	hypothetical protein	4.63e+00
14	61	60.4	860	7	\$55543	reverse transcriptase	4.63e+00
15	9	59.4	217	~	D64935	hypothetical protein	6.76e+00
16	59	58.4	102	~	E65040	hypothetical protein	9.83e+00
11	59	58.4	102	~	C64007	hypothetical protein	9.83e+00
18	59	58.4	296	~	A40593	transcription activat	9.83e+00
13	59	58.4	529	٦	AOHUBA	beta-N-acetylhexosami	9.83e+00
20	59	58.4	649	~	301515	dnaK-type molecular c	9.83e+00
71	58	57.4	341	N	826206	 hypothetical protein 	1.42e+01
22	58	57.4	528	~	148253	beta-N-acetylhexosami	1.42e+01
23	28	57.4	655	~	A42420	L-iduronidase (EC 3.2	1.42e+01

2.05e+01 2.05e+01 2.05e+01	2.05e+01 2.05e+01	2.05e+01 2.05e+01	2.05e+01 2.05e+01	2.95e+01 2.95e+01	2.95e+01 2.95e+01	2.95e+01 2.95e+01	2.95e+01 2.95e+01	2.95e+01	4.22e+01 4.22e+01
MSL leader peptide 2 hypothetical protein ornithine carbamovitr	hypothetical protein genome RNA2 protein -	hypothetical protein ovostatin precursor -	tenascin precursor - tenascin-C - human	erythromycin resistan hypothetical protein	MSL leader peptide 3 DNA adenine methylase	probable translation hypothetical protein	dnak-type molecular c	tenascin precursor -	alpha-amylase (EC 3.2 pisatin demethylase P
I39482 S28674 OWPSCA	H70573 WMVXCU	T01734 A20872	JQ1322 A32160	C25028 I40879	S49317 A27507	F71306 S31045	HHKW7A A45635	S19694	A55861 S34286
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43 238 336	493 857 857	878 1473	2019	4 4 W W	43	368	640 644	1746	504
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57.	57.	57	57 57	56 56	56 56	26 56	26 56	5. 0 1.	222
24 25 26	27 28 29	30	33 33	34 35	36 37	38 36 36	40	4243	44

ALIGNMENTS

ALTERRANTE_NAMES ANTITULED natituretic factor: atrial appa natituretic factor: atrial appare atrial appared atrial appared atrial appared atrial appared atrial appared atrial appared atrial atri	RESULT 1 ENTRY	AWHU *type complete
ANAMES ANF: atrial natriuretic factor; atrial natriuretic proper prepronatriodilatin (PND) atrial alpha natriuretic peptide (ANP); cardiodilatin atrial alpha natriuretic factor) ## Cornal Laname Homo sapiens # Common_name man is-Nov-1984 #text_chang 20-Mar-1984 #sequence_revision 15-Nov-1984 #text_chang 139458; 139458; 139459; 139460; 137167 **AZ2693; **AZ2693; **AZ2693 **AZ2693; **AZ2693; **AZ2693 **AZ2693;	TITLE	
atilal alpha natriuretic peptide (ANP); cardiodilatin gramma natriuretic factor) #formal_name Homo sapiens #common_name man is-Nov-1984 #text_chang 20-Mar-1998 *A22693; B22693; A01424; B29370; A32733; IS8054; S14097 A22693; B22693; A01424; B29370; A32733; IS8054; S14097 A22693; B22693; A01424; B29370; A32733; IS8054; S14097 A22693; Baner, M.; Chamberland, M.; Sirois, D.; Argentin, S.; J.; Dixon, R.A.F.; Zivin, R.A.; Condra, J.H. In Nature (1984) 312:654-656 Gene structure of human cardiac hormone precursor, promatriodilatin. references MUID:85061626 Sion A22693 A226933 A2269333 A226933 A226933 A2269333 A226933 A226933 A2269333 A2269333 A2269333 A2269333 A2269333 A2269333 A2269333 A226933 A2269333 A2269333 A2269333 A2269333 A2269333 A226933 A2269333 A226933 A226933 A2269333 A226933 A2269333 A226933 A2269333 A226933 A226933 A226933 A2269333 A226933 A22693 A226933 A226	ALTERNATE_NAMES	ANF; atrial natriuretic factor; prepronatriodilatin (PND)
#formal_name Homo sapiens #common_name man isformal_name Homo sapiens #common_name man is-Nov-1984 #text_chang 20-Mar.1998 A22693; B22693; A01424; B29370; A32733; ISB054; S14097 ISB458; I39468; I39469; I37167 A22693; B22693; A01424; B29370; A32733; ISB054; S14097 ISB458; I39469; I37167 A22693; B22693; A01424; B29370; A32733; ISB054; S14097 ISB42693 I Dixton, R.A.F.; Zuvin, R.A.; Condra, J.H. Hature (1984) 312:564-656 Gene structure of human cardiac hormone precursor, promatricodilatin. references MUID:85061626 Sion A22693 I-151 #flabel NEM	CONTAINS	
15-Nov-1984 #sequence_revision 15-Nov-1984 #text_chang 20-Mar-1998 8	ORGANISM	#common_name man
S A22693; B22693; A01424; B29370; A32733; I58054; S14097 139458; I39459; I39460; I37167 A22693 IS Remer, M.; Chamberland, M.; Sirois, D.; Argentin, S.; J.; Dixon, R.A.F.; Zuvin, R.A.; Condra, J.H. Hature (1984) 312:654-656 Gene structure of human cardiac hormone precursor, pronatriodilatin. references MUID:85061626 Sion A22693 Olecule_type DNA esidues 1-151 ##label NED CGA arginine codon A01424 CGA arginine codon A01424 CGA arginine codon A01424 I Rangawa, R.; Fukuda, A.; Matsuo, H. Rangawa, R.; Fukuda, A.; Matsuo, H. Alture (1984) 309:724-726 Cloning and sequence analysis of cDNA encoding a precurences MUID:84219799 Sion A01424 Cloning and sequence analysis of cDNA encoding a precure of human atrial natriuretic polypeptide. references MUID:84219799 I Rangawa, J.G. Seidman, C.E.; Bloch, K.D.; Klein, K.A.; Smith, J.A.; Seidman, C.E.; Bloch, C.E	DATE	sion 15-Nov-1984
N22693 Newer, M.; Chamberland, M.; Sirois, D.; Argentin, S.; J.; Dixon, R.A.F.; Zivin, R.A.; Condra, J.H. Hature (1984) 312:654-656 Gene structure of human cardiac hormone precursor, pronatricodiatin. Teferences MUD: 85061626 Sion A22693 1-151 ##label NEM Sion B22693 Clecule_type DNA esidues	ACCESSIONS	432733; ISB054;
Is Nemer, M.; Chamberland, M.; Sirois, D.; Argentin, S.; J. Dixon, R.A.F.; Zivin, R.A.; Condra, J.H. J. Dixon, R.A.F.; Zivin, R.A.; Condra, J.H. Nature (1984) 312:654-656 Gene structure of human cardiac hormone precursor, references MulD:85061626 sion A22693 olecule_type DNA residues 1-151 ##label NEM residues 1-151 ##label NEM residues 1-151 ##label NED ston #22693 ston #22693 colecule_type DNA residues allelic variant with UGA termination codon replace GGA arginine codon A01424 cGA arginine codon A01424 al Rangawa, R.; Fukuda, A.; Matsuo, H. Natzato, H.; Kangawa, R.; Fukuda, A.; Matsuo, H. Natzure (1984) 309:724-726 Cloning and sequence analysis of cDNA encoding a precufor human atrial natriuretic polypeptide. references MULD:84219799 slon A01424 cloning and sequence analysis of cDNA encoding a precufor human atrial natriuretic polypeptide. references MULD:84219799 slon A01424 clossing RESIDOCH, K.D.; Klein, K.A.; Smith, J.A.; Seidman, C.E.; Bloch, K.D.; Klein, K.A.; Smith, J.A.; Seidman, D.G. B29370 natriuretic factor genes.	REFERENCE	A22693
Hature (1984) 312:654-656 Gene Structure of human cardiac hormone precursor, pronatriodilatin. Teferences MUID:85061626 \$\text{ston}\$ \$\t	#authors	M.; Chamberland, M.; Sirois, D.; Argentin, S.; Dixon, R.A.F.; Zivin, R.A.; Condra, J.H.
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#formal_name Bos primigenius taurus #common_name cattle
30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change
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atrium; diuretic; hormone; natriuretic; osmoregulation
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#superfamily natriuretic peptide A precursor
atrium; diuretic; hormone; natriuretic; osmoregulation
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experimental #label ANP\
Nucleotide sequence of the gene encoding human atrial
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                                                                                                                                                                                                                                           not a diuretic
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                                                                                                                                                    ##molecule_type DNA
##residues 26-151 ##label RE5
##cross-references EMEL:X01471; NID:928690
rr Cardiodilantin is a vasoconstrictor but
natriuretic.
                                                                                                                            translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                            #gene GDB:NPPA; ANP; PND
##cross-references GDE:118727; OMIM:108780
#map_position 1p36-1p36
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A90124; A93049; A24247; A26090
                               natriuretic factor precursor.
#cross-references MUID:85061627
#accession I37167
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##residues 123-150 ##label ONG
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#cross-references MUID:85173941
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A50899
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#product gamma atrial natriuretic factor #status
predicted #label ANF\
#product alpha atrial natriuretic peptide #status
predicted #label ANP\
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                                                                                                                                                                                                                                                                                                                                                                                        S.; Imai, M.; Inuzuka, C.; Tawaragi, Y.; Nakazato,
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ANP; atrial natriuretic polypeptide
#formal_name Canis lupus familiaris #common_name dog
31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change
                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##residues 1-153 ##label OIK ##cross-references GB:M12046; NID:g164770; PID:g164771 CLASSIFICATION #superfamily natriuretic peptide A precursor KEYWORDS atrium; diuretic; hormone; natriuretic; osmoregulation
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#length 153 #molecular-weight 16843 #checksum 7650
#length 152 #molecular-weight 16518 #checksum 7552
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Pred. No. 1.10e-07;
0; Mismatches 0; Indels
                                Length 152;
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                                  Score 101; DB 1; Length 152
Pred. No. 1.10e-07;
0; Mismatches 0; Indels
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Structure of dog a
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*accession A25302
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                                                                                                                                                                                                                                                                                                                                                                                                           H.; Matsuo, H.
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Matches 15: Con-
                                  Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 15; Conservative
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#ittle Nucleotide sequence of a porcine prepro atrial natriuretic peptide (ANP) cDNA.
#cross-references MUID:91067478
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#product alnha atria.
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#product gamma atrial natriuretic factor #status
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#product alpha atrial natriuretic peptide #status
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Anat. Embryol. (1931) 168:307-313
The right auricle of the heart is an endocrine organ.
Cardiodilatin as a peptide hormone candidate.
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##residues 25-54 ##label FOR
FPICATION #superfamily natriuretic peptide A precursor
RDS atrium; diuretic; hormone; natriuretic; osmoregulation
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Pred. No. 4.64e-07;
1; Mismatches 0; Indels
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Pred. No. 4.64e-07;
1; Mismatches 0; Indels
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#length 150 #molecular-weight 16351 #c
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##residues 1-150 ##label MAE
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tcross-references MUID:85182558
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ANF(1-33); ANF(2-33); ANF(8-33); ANF(8-33);

natriuretic peptide; atriopeptin I: atriopeptin II;

auriculin A; auriculin B; preprocardionatrin

#formal_name Rattus norvegicus #common_name Norway rat

19-Feb-1984 #sequence_revision 15-Nov-1984 #text_change
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##cross-references EMBL:X58562: NID:g49543; PID:g49544
##experimental_source heart atria; adult
FICATION #superfamily natriuretic peptide A precursor
EICATION atrium; diuretic; hormone; natriuretic; osmoregulation
DS
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                                                                 H.J.; Hanke, M.; Schmeding, G.; Teuteberg,
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                                                                 Maegert, H.J.; Hanke, M.; Schmeding, G.; Teutel
Schulz-Knappe, P.; Forssmann, W.G.
submitted to the EMBL Data Library, March 1991
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Pred. No. 1.92e-06;
                                                                                                                                                                                                                                                                                                    Score 98; DB 2; Length 153; Pred. No. 4.64e-07; 1; Mismatches 0; Indels
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J. Biol. Chem. (1985) 260:4568-4571
The gene for rat atrial natriuretic factor.
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Matches 14; Conservative
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#authors Atlas, S.A.; Kleinert, H.D.; Camargo, M.J.; Januszewicz, A.; Fauthors Sealey, J.E.; Laragh, J.H.; Schilling, J.W.; Lewicki, J.A.; Johnson, L.K.; Maack, T. #journal Nature (1984) 309:717-719 #title Purification, sequencing and synthesis of natriuretic and vascactive rat atrial peptide. #cross-references NUID:84219796 #accession A93330
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                                                                                                                                                      #authors Yamanaka, M.; Greenberg, B.: Johnson, L.; Seilhamer, J.;
Brewer, M.; Friedemann, T.; Miller, J.; Atlas, S.; Laragh,
J.; Lewicki, J.; Fiddes, J.
#journal Nature (1984) 309:719-722
#title Cloning and sequence analysis of the cDNA for the rat atrial
#cross-references MUID:84219797
#accession A01425
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Lazure, C.; Chretien, M.; Cantin, M.
Peptides (1989) 9:47-53
NH2-terminal fragment of rat pro-atrial natriuretic facto
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#cross-references MUID:84250178
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##residues 1-152 ##label SEI
##cross-references GB:K02062; GB:K02063; NID:g202899; PID:g202900
SNCE A93330
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Tibbetts, C.; Inagami, T.
Nature (1984) 309:722-724
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##molecule_type protein
##residues
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##cross-references EMBL:X00665; NID:955711; PID:955712
#accession A22570
##moldecule_type DNA
##residues
##cross-references GB:K02062; NID:9202899; PID:9202900
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##residues 126-149 ##label ATL
:NCE A94275
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##residues 127-149 ##label CUR
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#cross-references MUID:84219798
#accession A93332
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#accession PT0061
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part of this sequence, including the amino ends of three mature peptides, was confirmed by protein sequencing
Seidah, N.G.; Lazure, C.; Chretien, M.; Thibault, G.; Garcia,
R.; Cantin, M.; Genest, J.; Nutt, R.F.; Brady, S.F.; Lyle,
T.A.; Paleveda, W.J.; Colton, C.D.; Ciccarone, T.M.; Veber,
D.F.
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Proc. Natl. Acad. Sci. U.S.A. (1987) 84:2175-2179
Identification of atrial natriuretic factor gene transcripts
in the central nervous system of the rat.
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The A disulfide bond is required for full activity of atriopeptins.
The Several active peptides may be derived from the carboxyl region of
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Protein Expr. Purif. (1990) 1.28-32
Purification of rat pro-atrial nariurelic factor: a
simplified scheme using reversed-phase high-performance
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Sakuragawa, Y.; Nakazato, H.; Fukuda, A.; Minamino, N.;
                                                                                                                                                                                                                                                                                                              Flynn, T.G.; Davies, P.L.; Kennedy, B.P.; de Bold, M.L.;
Bold, A.J.
Science (1985) 228:323-325
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                                                                                                    #journal Proc. Natl. Acad. Sci. U.S.A. (1984) #1:2640-2644
#title Amino acid sequence of homologous rat atrial peptides:
natriuretic activity of native and synthetic forms.
#cross-references MID: #41194062
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preliminary; translated from GB/EMBL/DDBJ
##molecule_type mRNA
##residues
1 1.52 ##label RE2
##cross.references EMBL:X01118; NID:955716; PID:955717
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##cross-references GB:R02062; NID:9202899; PID:9202900
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##cross-references GB:M15868; NID:9202903; PID:9202904
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##residues 118-150 ##label SE2
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tcross-references MUID:93044510
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#accession 159094
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#product atriopeptin II #status experimental #label AT2\
#disulide_bonds #status experimental
#length 152 #molecular-weight 16556 #checksum 7818
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#product ANF(3-33) #status experimental #label ANF2\
#product ANF(3-33) #status experimental #label ANF3\
#product cardionatrin I #status experimental #label CN
#product ANF(8-33) #status experimental #label ANF4\
#product ANF(8-33) #status experimental #label ANF4\
#product auriculin B #status experimental #label AUB\
#product auriculin A #status experimental #label AUB\
                                                                                                                            #domain signal sequence #status predicted #label SIG\
#product pro-atrial natriuretic factor #status
experimental #label PRO\
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predicted #label ANP\
#disulfide_bonds #status predicted
#length 152 #molecular-weight 16645 #checksum 9384
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#title Nucleotide sequences of the human and mouse atrial natriuretic factor genes.
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Pred. No. 1.92e-06;
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Best Local Similarity 86.7%;
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                                                                                      atrial natriuretic peptide precursor - bullfrog
ANP; atrial natriuretic factor (ANF)
atrial natriuretic peptide-21; atrial natriuretic peptide-24
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#domain propeptide #status predicted #label PRO\
#product atrial natriuretic peptide-24 #status
experimental #label M24\
#product atrial natriuretic peptide-21 #status
experimental #label M21\
#status predicted
#status predicted
#fisulfide_bonds #status predicted
#length 145 #molecular-weight 15934 #checksum 1892
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submitted to the EMBL Data Library, December 1994
Identification of the novel Drosophila melanogaster heat
shock gene, lethal(2)denticleless (1(2)dt1), coding for
                                                                                                                                                                                                                                                                                                                                                           Biochem. Biophys. Res. Commun. (1988) 155:1338-1345
Identification of new atrial natriuretic peptides in frog
                                                                                                                           #formal_name Rana catesbelana #common_name bullfrog
30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change
20-Mar-1998
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##residues 122-145 ##label SAK
IT In mammals, several active peptides may be derived from the
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Pred. No. 4.96e-05;
1; Mismatches 2;
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##cross-references FlyBase:FBgn0013548
                                                                         #type complete
                                                                                                                                                                                                                         #Authors Nojame to Jiric, and the submission submitted to Jiric, accession J00947
##molecule_type mRNA
##molecule_type TI45 ##label KOJ
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Best Local Similarity 80.0%;
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#formal_name Mycobacterium tuberculosis
17-Jul-1993 #sequence_revision 17-Jul-1998 #text_change
17-Jul-1993 #sequence_revision 17-Jul-1998 #text_change
17-Jul-1998
G70575
A70500
Cole, S.T.: Brosch, R.; Parkhill, J.; Garnier, T.; Churcher,
C.: Harris, D.; Gordon, S.V.; Eiglmeier, K.; Gas, S.; Barry
III, C.E.; Tekaia, F.; Badcock, K.; Basham, D.; Brown, D.;
Chillingworth, T.; Connor, R.; Davies, R.; Deviln, K.;
Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Moule, S.;
Murphy, L.; Oliver, S.; Osborne, J.; Quail, M.A.;
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                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein MTH1746 - Methanobacterium thermoautotrophicum (strain Delta H) # 605-Dec-1957 #sequence_revision 05-Dec-1997 #text_change 605-Unn-1998 # 60000
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Complete genome sequence of Methanobacterium
thermoautotrophicum Delta H: functional analysis
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#domain WD repeat homology #label WD1\
#domain WD repeat homology #label WD2
#length 758 #molecular-weight 82351 #checksum
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#length 196 #molecular-weight 21469 #checksum
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Pred. No. 6.56e-01;
"..matches 2; Indels
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                                                                                                                 65.3%;
larity 61.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 64.4%;
Best Local Similarity 53.3%;
Matches 8; Conservative
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| LRALLTAPRSLRRSS 15
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##status
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                                                                                                                             #journal
                                      #authors
 ACCESSIONS
REFERENCE
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34-41
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hypothetical protein b1756 - Escherichia coli (strain K-12)
#formal_mame Escherichia coli
12.5ep-1997 #sequence_revision 17-5ep-1997 #text_change
10-Jul-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   reverse transcriptase - fruit fly (Drosophila melanogaster)
#formal_name Drosophila melanogaster
27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to the EMBL Data
                                                                      Deciphering the biology of Mycobacterium tuberculosis from
                                                                                                                                                                                                ##residues 1-215 ##label COL
##cross-references GB:295324; GB:AL123456; NID:g3261760; PID:e315475;
PID:g2094839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #authors Udomkit, A.; Forbes, S.; Dalgleish, G.; Finnegan, D.J.
#journal Nucleic Acids Res. (1995) 23:1354-1358
#title BS a novel LINE-like element in Drosophila melanogaster.
#cross-references MUID:95273172
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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##cross-references FlyBase:FBgn0000224
# #length 860 #molecular-weight 98647 #checksum 4270
                                                                                                                                                                                                                                                                                                              #length 215 #molecular-weight 23102 #checksum 4474
                                                                                                                                           eliminary; nucleic acid sequence not shown; translation not shown
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red. No. 4.63e+00;
5; Mismatches 2
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                                                                                         the complete genome sequence #cross-references MUID:98295987
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                                                                                                                                                                                                                                                                                                                                                   Score 61;
Pred. No. 4
                   Skelton, S.; Squares, S.
Taylor, K.; Whitehead, S
Nature (1998) 393:537-544
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##cross-references EMBL:X77571
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                                                                                                                                             preliminary;
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ilarity 57.1%;
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ilarity 53.3%;
Conservative
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1 LRALLTAPRSLRRSS 15
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Matches 8; Conserv
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Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                              ##residues 1-217 ##label BLAT ##cross-references GB:AE000270; GB:U00096; NID:g1788045; PID:g1788053; UWGP:b1756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #domain ATP-binding cassette homology #label ABC\
#region nucleotide-binding motif A (P-loop)
#length 217 #molecular-weight 24016 #checksum 7949
                                                                                                                                                                        #title The complete genome sequence of Escherichia coli K-12.
#cross-references MUID:97426617
                                                                                                                                                                                                                                                            preliminary; nucleic acid sequence not shown; translation not shown
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Pred. No. 6.76e+00;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               ##experimental_source strain K-12, substrain MG1655
FICATION #Superfamily ATP-binding cassette homology
tbS
                                                                                                                                          Science (1997) 277:1453-1462
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                      ##molecule_type DNA
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Research Unit. Release 3.1A John F. Collins, Biocomputing Research Un. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein · protein database search, using Smith-Waterman algorithm MasPar time 2.25 Seconds 188.112 Million cell updates/sec MPsrch_pp

Wed Jun 16 13:19:41 1999; Run on:

Tabular output not generated.

>US-09-027-777B-2 (1-15) from US09027777B.pep 101 Description: Perfect Score: Title:

1 LRALLTAPRSLRRSS 15 Seguence:

PAM 150 Gap 15 Scoring table:

Searched:

77977 seqs, 28268293 residues

summaries Minimum Match 0% Listing first 45 Post-processing:

swiss-prot37 1:swissprot Database:

Mean 28.009; Variance 37.502; scale 0.747 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	2.41e-09	2.41e-09	2.41e-09	1.25e-08	1.25e-08	1.25e-08	6.41e-08	6.41e-08	6.41e-08	2.68e-06	1.38e-01	2.96e+00	4.51e+00	4.51e+00	4.51e+00	6.82e+00	6.82e+00						
Description	ATRIAL NATRIURETIC FAC	LETHAL(2)DENTICLELESS	HYPOTHETICAL 10.8 KD P	HYPOTHETICAL 11.6 KD P	HYPOTHETICAL PROTEIN H	UREASE OPERON TRANSCRI	NODULATION PROTEIN NOL	BETA-HEXOSAMINIDASE AL	HEAT SHOCK 70 KD PROTE	HYPOTHETICAL PROTEIN I	BETA-HEXOSAMINIDASE AL	ALPHA-L-IDURONIDASE PR	ORNITHINE CARBAMOYLIRA	PROBABLE RNA-DIRECTED									
ID	ANF_BOVIN	ANF_HUMAN	ANF_RABIT	ANF_CANFA	ANF_PIG	ANF_HORSE	ANF_CAVPO	ANF_MOUSE	ANF_RAT	ANF_RANCA	L2DT_DROME	YFJF_ECOLI	YFJF_VIBCH	YFJF_HAEIN	URER_ECOLI	NOLL_RHISN	HEXA_HUMAN	HS70_CHLRE	YGL1_STRCO	HEXA_MOUSE	IDUA_CANFA	OTCC_PSEAE	V2A_CMVNT
DB	-	-1	н	~	٦	П	٦	Н	Н	-	-	٦	٦	٦	-	-	-	٦	٦	П	ч	H	7
Length	152	153	153	149	150	153	128	152	152	145	758	96	101	102	296	366	529	649	341	528	655	335	857
% Query Match	100.0	100.0	100.0	97.0	97.0	97.0	94.1	94.1	94.1	87.1	65.3	58.4	58.4	58.4	58.4	58.4	58.4	58.4	57.4	57.4	57.4	56.4	56.4
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Result No.	-	7	٣	4	2	φ	7	80	6	10	11	12	13	14	15	16	17	18	19	. 50	21	22	23

ALIGNMENTS

RESULT ID A AC P	1 NF_BOVIN STA 07501;
555	01-APR-1988 (REL. 07, CREATED) 01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE) 01-CCT-1996 (REL. 34, LAST ANNORATION UPDATE)
DE	URETIC FACTOR E
N G	NPPA.
88	BOS TAURUS (BOVINE). EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
ဗ	ARTIODACTYLA; RUMINANTIA; PECORA; BOVOIDEA; BOVIDAE; BOVINAE; BOS.
N G	[1]
ž ž	MEDLINE: 86215205.
RA	P., MILLER J., BENCEN
RT	of the
Z 2	precursor gene."; prochem prophyc pec commin 136.306.403/1086)
Z.	
RP	SEQUENCE OF 123-150.
RX	MEDLINE; 86173941.
ΚA	ONG H., MCNICOLL N., LAZURE C., SEIDAH N., CHRETIEN M., CANTIN M.,
RA	
RT	"Purification and sequence determination of bovine atrial natriuretic
RŢ	factor.";
3 2	
38	-:- FUNCTION: AFKIAL MAININGTINE IN A FOTENT VASOACTIVE
38	SUBSTANCE SINIBESIDED IN MAMMALIAN AIKIA AND IS INCUGAI TO PLAI A KEY ROLE IN CARDIOVASCHIAR HOMEOSTASIS. HAS A CGMD-STIMHIATING
ខ	ACTIVITY:
႘	-!- A DISULFIÜE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS.
ပ္ပ	-!- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
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3 8	This SWISS-PROT entry is copyright. It is produced through a collaborate
3 5	between the SMISS institute of Bloinformatics and the Embi Outstat the Rutobean Nicinformatics Institute There are no restrictions on
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χ, c	EMBL; M13145; G162666; D1B: h3/3/7: hwd
Z Z	PROSITE: PS00263: NATRIURETIC PEPTIDE: 1
· DR	
ΚM	VASOACTIVE; SIGNAL.

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Molecular cloning and characterization of DNA sequences encoding rat
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MEDLINE: 850
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SEQUENCE
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PFAM; PF(
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13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-151 FROM N.A. MEDLINES 84219799.

MEDLINES 84219799.

OIKAWA S., IMAI M., UENO A., TANAKA S., NOGUCHI T., NAKAZATO H., KANGAWA K., FUKUDA A., MATSUO H.;

"Cloning and sequence analysis of cDNA encoding a precursor for human atrial natriuretic polypeptide.";

NATION 109:724-726(1984).
               ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP)
                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleotide sequence of the gene encoding human atrial natriuretic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAKAYAMA K., OHKUBO H., HIROSE T., INAYAMA S., NAKANISHI S.;
"mRNA sequence for human cardiodilatin-atrial natriuretic factor
precursor and regulation of precursor mRNA in rat atria.";
NATURE 310:699-701(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIVIN R.A., CONDRA J.H., DIXON R.A.F., SEIDAH N.G., CHRETIEN M.,
NEMER M., CHAMBERLAND M., DROUIN J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE: 85065766.
SEIDWAN C.E., BLOCH K.D., KLEIN K.A., SMITH J.A., SEIDWAN J.G.,
"Nucleotide sequences of the human and mouse atrial natriuretic
                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                     EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ь.
                                                                       Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEMER M., CHAMBERLAND M., SIROIS D., ARGENTIN S., DROUIN DIXON R.A.F., ZIVIN R.A., CONDRA J.H.; "Gene structure of human cardiac hormone precursor, pronatriodilatin."; NATURE 312:654-656(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GREENBERG B.D., BENCEN G.H., SEILHAMER J.J., LEWICKI J.A.
                                                                                                     0; Indels
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                                                                       Score 101; DB 1; I
Pred. No. 2.41e-09;
0; Mismatches 0;
   1 24
123 150 ATRIAL NATRIURETI
129 145
152 AA: 16518 MW: CF200882 CRC32;
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                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 118-153 FROM N.A. MEDLINE; 85038509.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCIENCE 226:1206-1209(1984).
                                                                                                                                                                                                                                                                                                            (PREPRONATRIODILATIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-151 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQUENCE OF 1-151 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-151 FROM N.A. 4EDLINE; 85061627.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-151 FROM N.A.
                                                                       100.0%;
larity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-151 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          factor precursor.";
ATURE 312:656-658(1984).
                                                                                                                                  114 LRALLTAPRSLRRSS 128
                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                             1 LRALLTAPRSLRRSS 15
                                                                                                                                                                                                                                                                                                                          NPPA OR PND.
HOMO SAPIENS (HUMAN).
                                                                       Query Match
Best Local Similarity
Matches 15; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 85061626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 84295577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'IDDES J.C.;
                                                                                                                                                                                                    LT 2
ANF_HUMAN
 SIGNAL
PEPTIDE
DISULFID
SEQUENCE
                                                                                                                                                                                                       RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTIVITY.

--- THE HUMAN GENOME CCNTAINS 2 DIFFERENT PREPRONATRIODILATIN GENES ONE CODES FOR 2 ARG RESIDUES AT THE C-TERMINUS THAT ARE CLEAVED TO FORM THE MATURE PEPTIOE, WHILE THE OTHER ENDS IN A TERMINATION CODON IMMEDIATELY AFTER THE LAST CODON OF THE MATURE PEPTIDE.

--- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
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BY SIMILARITY.
MISSING (IN ONE OF THE TWO GENES).
C24A68AF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY REY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
                                                                                                                                                                                                                                                                                                                     MEDIAINE; 0412013.
RANGAMA K., MATSOV H.;
RANGAMA K., NATSOV H.;
PUTIFICATION and complete amino acid sequence of alpha-human atrial
natriuretic polypeptide (alpha-hANP).";
BIOCHEM. BIOPHYS. RES. COMMUN. 118:131-139(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARDIODILATIN-RELATED PEPTIDE (CDP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 94318633.
FAIRBROTHER W.J., MCDOWELL R.S., CUNNINGHAM B.C.;
"Solution conformation of an atrial natriuretic peptide variant
selective for the type A receptor.";
BIOCHEMISTRY 33:8897-8904(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRUCTURE BY NMR OF 124-151 MUTANT SELECTIVE FOR NPR-C RECEPTOR
                                                                                                                    MEDLINE; 85096983.
MAKI M., PARKENTIER M., INAGAMI T.;
"CLoning of genoue DNA for human atrial natriuretic factor.";
BIOCHEM. BIOPHYS. RES. COMMUN. 125:797-802(1984).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 101; DB 1; Length 153
Pred. No. 2.41e-09;
0; Mismatches 0; Indels
and human atrial natriuretic factors.";
PROC. NATL. ACAD. SCI. U.S.A. 81:6325-6329(1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; PS00263; NATRIURETIC_PEPTIDE; 1.
PP00212; ANP: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X01470; G825625; -.
EMBL; X02558; G825625; JOINED.
EMBL; X02043; G178630; -.
EMBL; X01471; E27452; ALT_SEQ.
EMBL; K02044; G178632; -.
EMBL; ALO21155; E1294859; -.
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151 r
146
153
16708 MW; '
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Best Local Similarity 100.0%;
Matches 15; Conservative
                                                                                           1-75 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; ALO21155; E1294859;
EMBL; M30262; G180182; -.
EMBL; K02399; G178634; -.
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152
153 AA;
                                                                                                                                                                                                                                                                            SEQUENCE OF 124-151.
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01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
                                                                     07, CREATED)
07, LAST SEQUENCE UPDATE)
34, LAST ANNOTATION UPDATE)
C FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between the Swiss Institute of Bioinformatics and the EMBL outstati
the European Bioinformatics Institute. There are no restrictions on
use by non-profit institutions as long as its content is in no
modified and this statement is not removed. Usage by and for commer
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-!- FUNCTION: ATRIAL NATRIAL NATRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS. SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
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                                                                                                                                                                                                                          ORYCTOLAGUS CUNICULUS (RABBIT).
EUKARYOTA: META2OA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
LAGOMORPHA; LEPORIDAE; ORYCTOLAGUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CANIS FAMILIARIS (DOG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
CARNIVORA; FISSIPEDIA; CANIDAE; CANIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 101; DB 1; 1
Pred. No. 2.41e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      153 AA; 16843 MW; 1FA4FB42 CRC32;
                        153 AA.
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0; Mismatches
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PROSITE; PS00265; NATRIURETIC_PEPTIDE; 1.
PFAM: PF00212; ANP; 1.
VASOACTIVE; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                        PRT;
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                        STANDARD;
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                                                                                                                             01-OCT-1996 (REL. 3
ATRIAL NATRIURETIC
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE; 86076957.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTIVITY
                                                  P07500;
01-APR-1988
                                                                                                01-APR-1988
01-OCT-1996
                     ANF_RABIT
P07500;
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RESULT
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01-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CELL TISSUE RES. 238:425-430(1984).
-!- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASCACTIVE
SUBSTANCE: SYNTHESIZED IN MAMBALIAN ATRIA AND IS THOUGHT TO PLAY A
KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-HEART RIGHT ATRIUM;
MEDLINE; 85124561.
FORSSMANN W.G., BIRR C., CARLQUIST M., CHRISTMANN M., FINKE R.,
HENSCHEN A., HOCK D., KIRCHHEIM H., KREYE V., LOTTSPEICH F., METZ J.,
MUTT V., REINECKE M.;
"The auricular myocardiocytes of the heart constitute an endocrine
organ. Characterization of a porcine cardiac peptide hormone,
                                                                                                                                                                                                                                                                                                                                                       ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 91067478.
MAEGERT H.J., APPELHANS H., GASSEN H.G., FORSSMANN W.G.;
"Nucleotide sequence of a porcine prepro atrial natriuretic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS.
                                                     ATRIOPEPTINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EUKARYOTA; METAŽOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
ARTIODACTYLA; SUIFORMES; SUINA; SUIDAE; SUS.
                                                   A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOI SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 98; DB 1; Le
Pred. No. 1.25e-08;
                                                                                                                                                                                                                                                                                                                                                                                              15819 MW; D4F3A6CF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                   PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1. PFAM; PF00212; ANP; 1.
                                                                                                                                                                                                               or send an email to license@isb-sib.ch)
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01-MAR-1992 (REL. 21, LAST SEQ)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PISSUE-HEART RIGHT ATRIUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                 97.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Conservative
                                                                                                                                                                                                                                                  EMBL; M12045; G163901; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 LRALLAAPRSLRRSS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VASOACTIVE; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 25-150.
                                                                                                                                                                                                                                                                                                                                                                                              149 AA;
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                                                                                                                                                                                                                                                                      A25302;
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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P24259;
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                                                                                                                                                                                                                                                                                                                     CARDIODILATIN-RELATED PEPTIDE (CDP)
(BY SIMILARITY).
ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
SY SIMILARITY.
; 4FF67B94 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAEGERT H.J., RICHTER R., SCHMAEDING G., FORSSMANN W.G.;
SUBNITTED (MAR-1991) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANT) IS A POTENT VASOACTIVE
SUBSTANCE SYNTHEBIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY
KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
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BY SIMILARITY.
FESDSF4A CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1992 (REL. 23, CREATED)
01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
ATRIAL NATRIGRETIC FACTOR PECURSOR (ANF) (ATRIAL NATRIURETIC (ANP) (PREPRONATRIODILATIN).
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PERISSODACTYLA; EQUIDAE; EQUUS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 98; DB 1; Length 150;
Pred. No. 1.25e-08;
1; Mismatches 0; Indels
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Pred. No. 1.25e-08;
1; Mismatches 0;
                                                                                                                                                                                                 PIR; S13107; S13107.
PROSITE: PSO0263; NATRIURETIC_PEPTIDE; 1.
PFAM; PF00212; AND; 1.
VASOACTIVE: SIGNAL.
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PROSITE; PSO0263; NATRIURETIC_PEPTIDE; 1.
PFAM; PFO0212; ANP; 1.
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16351 MW;
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larity 93.3%;
Conservative
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93.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 LRALLAAPRSLRRSS 128
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151
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                                                                                                                                                                       EMBL; X54669; G1884; -.
                                                                                                                                                                                                                                                                                                                                                                        123
129
150 AA;
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Best Local Similarity
Matches 14; Conser
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les 14; Conser
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P27104;
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SEQUENCE
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Gaps

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Indels

Conservative

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P05123.
13-AUG-1987 (REL. 05, CREATED)
13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
(ANP) (PREPRONATRIODILATIN).
                                                                                                                                                                                                                                                     01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
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ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
BY SIMILARITY.
2C2F552D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-HEART ATRIUM;
MAEGERT H.J., HANKE M., SCHMEDING G., TEUTEBERG K.,
SCHULZ-KNAPPE P., FORSEMANN W.G.;
SCHULZ-KNAPPE P., TORSEMANN W.G.;
SUBMITTED (MAR-1991) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANT) IS A POTENT VASOACTIVE
SUBSTANCE SYNTHESIZE IN NAMAALIAN AND IS THOUGHT TO PLAY A
KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
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    -!- DEVELOPMENTAL STAGE: ADULT.
    -!- A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS.
    -!- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.

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RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                              EUKARYOTA; METAZÓA; CHÓRDATÀ; VERTEBRATA; MAMMALIA; EUTHERIA.
RODENTIA; HYSTRICOGNATHI; CAVIIDAE; CAVIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 128
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Pred. No. 6.41e-08;
0; Mismatches 1.
                                                                                                                                                                        128 AA
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PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
PFAM: PF00212; ANP; 1.
VASOACTIVE.
                                                                                                                                                                                                                                                                                                                                              (ANP) (PREPRONATRIODILATIN) (FRAGMENT).
                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                 23, CREATED)
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                                                                                                                                                                                                                                                                                                                                                                                                      PORCELLUS (GUINER PIG).
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126
121
13966 M
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14; Conservative
EMBL; X58562; G49544; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90 LRALLDAPRSLRRSS 104
                                                                                                                                                                        STANDARD;
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EUKARYOTA: METAZOA: C
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105 1
128 AA;
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SEQUENCE FROM N.A.
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01-AUG-1992
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P27596;
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PEPTIDE
PEPTIDE
DISULFID
SEQUENCE
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SEIDAH N.G., LAZURE C., CHRETIEN M., THIBAULT G., GARCIA R., CANTIN M., GENEST J., NUTT R.F., BRADY S.F., LYLE T.A., PALEVEDA W.J., COLTON C.D., CICCARONE T.M., VEBER D.F., "Amino acid sequence of homologous rat atrial peptides: natriuretic activity of native and synthetic forms.";

PROC. NATL. ACAD. SCI. U.S.A. 81:2640-2644(1984).
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PROC. NATL. ACAD. SCI. U.S.A. 81:6325-6329(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATLAS S.A., KLEINERT H.D., CAMARGO M.J., JANUSZEWICZ A., SEALEY J.E., LARAGH J.H., SCHILLING J.W., LEWICKI J.A., JOHNSON L.K., MAACK T.; "Purification, sequencing and synthesis of natriuretic and vasoactive rat atrial peptide."; nature 309:717-719(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The elucidation of the structure of atrial natriuretic factor, a new peptide hormone.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GARDNER D.G., VLASUK G.P., BAXTER J.D., FIDDES J.C., LEWICKI J.A.; "Identification of atrial natriuretic factor gene transcripts in the central nervous system of the rat."; PROC. NATL. ACAD. SCI. U.S.A. 84:2175-2179(1987).
                                   SEIDMAN C.E., DUBY A.D., CHOI E., GRAHAM R.M., HABER E., HOMCY C., SMITH J.A., SEIDMAN J.G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRIE M.G., GELLER D.M., COLE B.R., SIEGEL N.R., FOK K.F., ADAMS S.P., EUBANKS S.R., GALLUPPI G.R., NEEDLEMAN P.; "Purification and sequence analysis of bioactive atrial peptides
                                                                                                                                                                                                                           NAKAZATO H., FUKUDA A., MINAMINO N., MATSUO H.;
"Identification of rat gamma atrial natriuretic polypeptide and
characterization of the CDNA encoding its precursor.";
NATURE 312:152-155(1984).
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MEDLINE; 88203350.
THIBAULT G., MÜRTHY K.K., GUTKOMSKA J., SEIDAH N.G., LAZURE C.,
                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 85182558.
ARGENTIN S., NEMER M., DROUIN J., SCOTT G.K., KENNEDY B.P.,
                                                                                                                                                                                                        KANGAWA K., TAWARAGI Y., OIKAWA S., MIZUNO A., SAKURAGAWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAN. J. PHYSIOL. PHARMACOL. 65:2013-2020(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                           "The gene for rat atrial natriuretic factor.";
J. BIOL. CHEM. 260:4568-4571(1985).
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SEQUENCE FROM N.A. MEDLINE; 84256178.
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85182558.
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                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
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21-JUL-1986 (REL. 07, LAST SEQUENCE UPDATE)
15-DEC-1986 (REL. 37, LAST ANNOTATION UPDATE)
ATRIAL NATRURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRURETIC PEPTIDE)
(ANP) (PREPRONATRIODILATIN) [CONTAINS: AURICULINS; ATRIOPEPTINS].
                                                                                                                             Ø
                                                         factor genes.";
SCIENCE 226:1206-1209(1984).
-!- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE
SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
KEY FOLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                  A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS. SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Structure of rat atrial natriuretic factor precursor deduced from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Σ
                   SEIDMAN C.E., BLOCH K.D., KLEIN K.A., SMITH J.A., SEIDMAN J.G.; "Nucleotide sequences of the human and mouse atrial natriuretic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 84219797.
YAMANAKA M., GREENBERG B., JOHNSON L., SEILHAMER J.J., BREWER FRIEDEMANN T., MILLER J., ATLAS S.A., LARAGH J., LEWICKI J., FIDDES J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 84219798.
MAKI M., TAKAYANAGI R., MISONO K.S., PANDEY K.N., TIBBETTS C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning and sequence analysis of the cDNA for the rat atrial natriuretic factor precursor.";
NATURE 309:719-722(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUKARYOTA; METAZOA; CHÓRDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AURICULIN A (BY SIMILARITY).
AURICULIN B (BY SIMILARITY).
ATRIOPEPTIN I (BY SIMILARITY).
ATRIOPEPTIN II (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          red. No. 6.41e-08;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5163CB23 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 95; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
PFAM; PF00212; ANP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16645 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 94.1%;
Best Local Similarity 86.7%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; K02781; G387099; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 LRALLAGPRSLRRSS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA sequence.";
NATURE 309:722-724(1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LRALLTAPRSLRRSS 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RATTUS NORVEGICUS (RAT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGI:97367; NPPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126
126
127
127
129
152 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VASOACTIVE; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A29370; AWMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
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PEPTIDE
DISULFID
SEQUENCE
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P01161;
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RESULT

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L2DT_DROME 024371;
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                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBD outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                        A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS. SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1990 (REL. 16, CREATED)
01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOYATION UPDATE)
ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
         "NH2-terminal fragment of rat pro-atrial natriuretic factor in the circulation: identification, radioimmunoassay and half-life."; peprides 9:47-53(1988).
-!- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMPHIBIA; BATRACHIA; ANURA;
RANA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-HEART;
MEDILIRE; 89025806.

MEDILIRE; 89025806.

"Identification of new atrial natriuretic peptides in frog heart.";
BIOCHEN, BIOCHEN, EDOPHYS. RES. COMMUN. 155:1338-1345(1988).

-I FUNCTION: VASCACTIVE ACTIVITY. HAS A CGMP-STIMULATING ACTIVITY.

-I SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 95; DB 1; Length 152; Pred. No. 6.41e-08; 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KOJIMA M.;
SUBMITTED (XXX-1992) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                     16556 MW; 2D424B75 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                               ATRIOPEPTIN III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 AA.
                                                                                                                                                                                                                                                                                                                                                                       ATRIOPEPTIN I.
ATRIOPEPTIN II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
NEOBATRACHIA; RANOIDEA; RANIDAE; RANINAE;
                                                                                                                                                                                                                                                                          PIR: A22570; AWRT.
PIR: A44190; A44190.
ROSJIE; PS00263; NATRIURETIC_PEPTIDE; 1.
PFAM: PF00212; ANP: 1.
VASOACTIVE: SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RANA CATESBEIANA (BULL FROG).
                                                                                                                                                                                                                                                                                                                                                                                                                                         94.1%;
86.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 86.7%;
Matches 13; Conservative
                                                                                                                                                                                                                    EMBL; M15868; G202904; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 LRALLAGPRSLRRSS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                            X00665; G55712; -. K02062; G202900; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LRALLTAPRSLRRSS 15
                                                                                                                                                                                                                                                                  M27498; G202906;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
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ANF_RANCA
P18909;
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PEPTIDE
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DISULFID
SEQUENCE
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                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KURZIK DUMKE U., NEUBAUER M., DEBES A.;

"Identification of a novel Drosophila melanogaster heat-shock gene,
"Identification of a novel Drosophila melanogaster heat-shock gene,
"Identification of a novel Drosophila melanogaster heat-shock gene,
"Identification of a novel Drosophila melanogaster heat-shock gene II: 1: 163-170(1996).

-! SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
-! TSUE SEPECIFICITY IN EXPRESSION UP TO STAGE II:
- NATH NO SIGN OF TISSUE SPECIFICITY IN EXPRESSION UP TO STAGE II:
- DEVELOPMENTAL STAGE: DETECTED AT ALL DEVELOPMENTAL STAGES. THE
EXTREMELY HIGH LEVEL OF TRANSCRIPTION DETECTED IN THE EARLY EMBRYO
AND IN ADULTS IS CAUSED BY MATERNAL MESSAGE.
-!- INDUCTION: BY HEAT SHOCK.
-!- SIMILARITY: CONTAINS 6 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRACHEATA; HEXAPODA; INSECTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
LETHAL(2)DEWICELESS PROTEIN (DIL83 PROTEIN).
L(2)DTL OR DTL83.
ENGSOPHILA MELANOGASTER (FRUIT FLY).
EUKARYOTA, METAZOA, ARTHROPODA; TRACHEATA, HEXAPODA; INSEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATRIAL NATRIURETIC FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 88; DB 1; Ler
Pred. No. 2.68e-06;
1; Mismatches 2;
   the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141
15934 MW; 6A1FA352 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       758 AA
                                                                                                                                                                                                                                                                    PIR; A31510; A31510.
PIR; JQ0947; JQ0947.
PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
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PROSITE; PS00678; WD_REPEATS; 1.
PFAM; PF00400; G-beta; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HEAT SHOCK; REPEAT; WD REPEAT
REPEAT 132 163 W
REPEAT 182 238 W
REPEAT 253 292 W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.1%;
llarity 80.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DROSOPHILIDAE; DROSOPHILA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 LRELLNAPRSMRRSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                     EMBL; D01043; D1001314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LRALLTAPRSLRRSS 15
                                                                                                                                                                                                                                                                                                                                                                   PFAM; PF00212; ANP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 96257214.
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                                                                                                                           Gaps
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SEQUENCE FROM N.A.
STRAIN-KIZ / MG1655;
MEDLINE: 97426617
BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,
BLATTNER F.R., COLLADO-YIDES J., GLASNER F.D., RODE C.K., MAXHEW G.F.,
GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
MAU B., SHAO Y.;
                                                                                                                                                                                                                       T 12
PYSTE_ECOLI STANDARD; PRT; 96 AA.
PYSTE_ECOLI STANDARD;
PYSTO 1996 (REL. 34, CREATED)
O1-CCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
O1-NOV-1997 (REL. 35, LAST ANDATION UPDATE)
HYPOTHETICAL 10.8 KD PROTEIN IN SMPA-SMPB INTERGENIC REGION (F102).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AIBA H., BABA T., FUJITA K., HAYASHI K., HONJO A., HORIUCHI T., IKEMOTO K., INADA T., ISONO K., ISONO S., ITOH T., KANAI K., KASAI H., KASHIMOTO K., KIM S., KIMUBA S., KITAKAWA M., MAKINO K., MASUDA S., MIKI T., MIZOBUCHI K., MORI H., MOTOWURA K., NAKAMURA Y., NASHIMOTO H., NISHIO Y., OSHIMA T., SAITO N., SAMPEI G., SEKI Y., TAGAMI H., TAKEMOTO K., WADA C., YAMAMOTO Y., YANO M.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-K12;
MEDLINE: 95023883.
KOMINE Y., KITABATAKE M., YOKOGAWA T., NISHIKAWA K., INOKUCHI H.;
"A tRNA-like structure is present in 105a RNA, a small stable RNA from Escherichia coli''':
                                                                                                                                                                                                                                                                                                                                   ESCHERICHIA COLI.
BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
ESCHERICHIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROC. NATL. ACAD. SCI. U.S.A. 91:9223-9227(1994).
-!- SIMILARITY: STRONG, TO H.INFLUENZAE HI0395.
                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete genome sequence of Escherichia coli K-12."; SCIENCE 277:1453-1474(1997).
                                                                                            Score 66; DB 1; Length 758;
Pred. No. 1.38e-01;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                  8F37E148 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96 AA; 10789 MW; F8707FB4 CRC32;
WD5.
WD6.
POLY-ALA.
POLY-GLY.
POLY-THR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAND DISSOL: SANDOTHELLE DISSOL: SEQUENCE 96 FT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U36840; G1033114; ALT_INIT.
EMBL; AE000347; G1788971; ALT_INIT.
EMBL; D90888; G1800023; -.
                                                                  82352 MW;
                                                                                             65.3%;
                                                                                                           larity 61.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-20 FROM N.A.
338
382
567
675
                                                                                                                                                    425 LRDLESTPRSLKR 437
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| LRALLTAPRSLRR 13
                                                                                                        Best Local Similarity
Matches 8: Conserv
                                                                  758 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-K12
                                                                   SEQUENCE
                                                                                              Query Match
 REPEAT
                           DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
HYPOTHETICAL 11.6 KD PROTEIN IN SMPA-SMPB INTERGENIC REGION (ORF101).
VIBRIO CHOLERAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F., KERLAVAGE A.R., MERRICK J.M., MCKENNEY B.A., MERRICK J.M., MCKENNEY B.A., MCKENNEY B.A., MCKENNEY B.A., MCKENNEY B.A., MCKENNEY R., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D., WELDMAN J.F., SHIRLEY R., LU L.-I., GLODEK A., KELLEY J.M., WELDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D., UTTERBACK T.R., HANNA M.C., FUGUYEN D.T., SAUDEK D.M., BRANDON R.C., FINE L.D., FRÄTCHMAN J.L., FUHRWANN J.L., GEOGHAGEN N.S.M., GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
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                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-OGAWA 395;
KOVACH M.E., HUGHES K.J., HARKEY C.W., EVERISS K.D., SHAFFER M.D.,
PETERSON K.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; VIBRIONACEAE; VIBRIO
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BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PASTEURELLACEAE;
HAEMOPHILUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VENTER J.C.; "whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 59; DB 1; Length 101; Pred. No. 2.96e+00; 4; Mismatches 2; Indels
                                                                                  Indels
Length 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBMITTED (OCT-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
Score 59; DB 1; L
Pred. No. 2.96e+00;
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01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
HYPOTHETICAL PROTEIN H10395.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 AA.
                                                                                  4; Mismatches
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Best Local Similarity 50.0%;
Query Match 58.4%;
Best Local Similarity 50.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U39068; G1100886; -. HYPOTHETICAL PROTEIN.
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STRAIN-RD / KW20;
MEDLINE; 95350630.
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                                                                                                                                                                                                                                                                                                                                                                                  LT 13
YFJF_VIBCH
P52120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YFJF_HAEIN
P43994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation her Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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D'ORAZIO S.E.F., COLLINS C.M.;
D'ORAZIO S.E.F., COLLINS C.M.;
The plasmid-encoded urease gene cluster of the family
Enterobacteriaceae is positively regulated by UreR, a member of the
AraC family of transcriptional activators.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                · I - SIMILARITY: BELONGS TO THE ARAC/XYLS FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. BACTERIÓL. 175:3459-3467(1993).
-i- FUNCTION: POSITIVE REGULATOR OF THE EXPRESSION OF THE UREASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
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PROSITE: PS00041; HTH.ARAC_FAMILY_1; 1.
PFOSITE: PS01124; HTH_ARAC_FAMILY_2; 1.
PFAM: PF00165; HTH_2: 1.
PFAM: PF00165; HTH_2: 1.
DFAM: PF00165; HTH_2: 1.
DFAM: PROSITE: PS01124; HTH_2: 1.
DFAM: PS0116; HTH_2: 1.
DFAM: PS0116; HTH_2: 1.
DFAM: PS0116; HTH_2: 1.
DFAM: PS0116; PS0116; PLASMID.
SEQUENCE 296 AA: 34032 MW; B99B2786 CRC32:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 59; DB 1; Length 102;
Pred. No. 2.96e+00;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           102 AA; 11584 MW; 1B2632C6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1993 (REL. 27, CREATED)
01-OCT-1993 (REL. 27, LAST SEDUENCE UPDATE)
11-OVY-1997 (REL. 35, LAST ANNOTATION UPDATE)
UREASE OPERON TRANSCRIPTIONAL ACTIVATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   296 AA
SCIENCE 269:496-512(1995).
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Best Local Similarity 50.0%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL PROTEIN.
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2 RALLTAPRSLRR 13
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URER_ECOLI
P32326;
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Gaps

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192 KALFTTPSTLRR 203

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2 RALLTAPRSLRR 13
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Search completed: Wed Jun 16 13:19:48 1999 Job time: 7 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

MasPar time 4.58 Seconds 178.668 Million cell updates/seq Wed Jun 16 13:20:04 1999; Run on:

Tabular output not generated.

>US-09-027-777B-2 (1-15) from US09027777B.pep 101

1 LRALLTAPRSLRRSS 15 Title: Description: Perfect Score: Seguence:

PAM 150 Gap 15 Scoring table:

179066 seqs, 54579741 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

sptremp19 Database:

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_nammal 7:sp_mhc 8:sp_organelle 5:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

Mean 26.978; Variance 38.734; scale 0.697

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Pred. No.		1.40e-08	1.40e-08	5.26e-07	
	Description P	***************************************	ATRIAL NATRIURETIC FAC 1.40e-08	ATRIAL NATRIURETIC PEP 1.40e-08	CARDIODILATIN, ATRIAL	
	ID		013766	152 6 046540	029130	
	98		4	9	9	
	Length		151	152	155	
Query	No. Score Match Length DB ID		101 100.0	101 100.0	93.1	
	Score		101	101	94	
Result	NO.		1	7	m	

Pred. No.	1.40e-08	1.40e-08	5.26e-07	5.20e-01	1.22e+00	2.83e+00	2.83e+00	2.83e+00	4.28e+00	4.28e+00	4.28e+00	6.44e+00	6.44e+00	6.44e+00	6.44e+00	6.44e+00	6.44e+00	6.44e+00	9.64e+00	9.64e+00
Description	ATRIAL NATRIURETIC FAC	ATRIAL NATRIURETIC PEP	CARDIODILATIN, ATRIAL	CYTOCHROME C-TYPE BIOG	VALYL TRNA SYNTHETASE.	HYPOTHETICAL 23.1 KD P	70-KDA HEAT SHOCK PROT	GLUCOSYLTRANSFERASE I	INNER MEMBRANE PROTEIN	KINASE.	ORF UL150.	R12E2.11 PROTEIN.	MAP KINASE KINASE ALPH	MAP KINASE KINASE 5.	ANGIOTENSIN/VASOPRESSI	ENVELOPE GLYCOPROTEIN.	ENVELOPE GLYCOPROTEIN.	SEMAPHORIN G PRECURSOR	MAP KINASE KINASE 4.	F58G6.1 PROTEIN.
ID	013766	046540	029130	027778	077443	006308	P97981	033426	P76909	052554	068404	061190	096517	080398	075434	073295	073299	060519	080397	021004
DB	7	9	9	7	S	~	12	~	~	7	14	S	10	10	4	14	14	11	10	2
Ouery Match Length	151	152	155	196	1218	215	216	373	246	303	642	227	348	348	514	856	856	1093	366	461
Query Match	100.0	100.0	93.1	64.4	62.4	60.4	60.4	60.4	59.4	59.4	59.4	58.4	58.4	58.4	58.4	58.4	58.4	58.4	57.4	57.4
Score	101	101	94	65	63	61	61	61	09	09	9	59	59	59	29	59	59	29	28	28
Result No.	-	7	m	ಶ	S	9	7	6 0	σ	10	11	12	13	14	15	16	17	18	19	20

9.64e+00 9.64e+00 9.64e+00 9.64e+00 1.44e+01 1.44e+	10.00
HEXOSAMINIDASE A (BETA SALI MODIFICATION METH ENVELODE GLYCORPOTEIN PEPTIDE SYNTHASE. PLASMID PIP501 COPR, R LCRABCDE GENES, COMPLE ORB. HYPOTHETICAL 53.0 KD P 2A PROTEIN. CMY-SD 2A. SIMILARITY TO MEMBRANE REVERSE GYRASE. KIAAO147 PROTEIN. PLASMID PAM-BETAL ADEN HYPOTHETICAL 4.8 KD PR HYPOTHETICAL 25.8 KD P BUTATIVE ABC TRANSPORT ENVELOPE GLYCOPROTEIN TENACIN PRECURSOR (TN JOHNSON GPASS ANCALCY NICHARCH CONTENT CONTENT OF THE STATE AD A DEN TOWN CAPASS ANCALCY NICHARCH CONTENT OF THE STATE AD A DEN TOWN CAPASS ANCALCY NICHARCH CAPA	- Student decorp modulion
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ALIGNMENTS

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								EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;					SEIDMAN C.E., BLOCH K.D., ZISFEIN J., SMIT J., HABER E., HOMCY C.,										P).	ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).					Gaps	
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				6	(TE)	•		JA;					IABE		"Molecular studies of the atrial natriuretic factor gene.";								CARDIODILATIN-RELATED PEPTIDE (CDP).	PEP			, Du	Pred. No. 1.40e-08:	0; Indels	
				01, LAST SEQUENCE UPDATE)	(TREMBLREL. 09, LAST ANNOTATION UPDATE)			MMAI							fac								ELAT	TIC		2;	-		ö	
	151 AA.			E UP	NOI			. WA					II J	DUBY A.D., CHOI E., GRAHAM R.M., SEIDMAN J.G.;	etic								IN-R	IURE	ľ.	E8827DA3 CRC32;	A 4	10e-	səc	
	151			JENC	TAT			MATA					SM	MAN	iur				PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1				LAT	MATR	BY SIMILARITY	A3 (-	, -	0; Mismatches	
			ED)	SEO	ANN	og.		TEBF					,	SEIL	natr				TIDE				IODI	AI.	IMI	827L	101	Ş	Misn	
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	۲;		(TREMBLREL. 01, CREATED)	. 01	. 0	ATRIAL NATRIURETIC FACTOR PRECURSOR.		ORDA	HOM				, G	AHAM	the	985)		EMBL; M54951; G178638; JOINED.	IURE							16381 MW;	100.08:	6	ive	
	PRELIMINARY;		REL	TREMBLREL.	REL	FAC	?	Š	DAE;				×	83	ų	34 (1	38;	38;	VATR	ä	_	25	55	151	146	16	100	100	vat	
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	PRE		T.	_	_	IURE	HOMO SAPIENS (HUMAN).	META	HOH		S	2062	<u>т</u>	CHOIL	stud	 7	EMBL; M54947; G178638;	1; 6	0026	PFAM; PF00212; ANP; 1:	VASOACTIVE; SIGNAL.	:	26	124	130	151 AA;		ilar	15; Conservative	
			9661	9661	01-JAN-1999	VATR	PIEN	[A;	(NI;		F	82	C.E	;	ar	SIO	494	3495	PS	2002	IVE;				_		_	Sim	15;	
٦	99	99	-VO	0.4	AN-1	AL 1	SAF	RYO	RRHI		ENCE	INE;	MAN	A.	ecn	RTEN	χ.,	E	ITE;	H.	ACTI	AL	IDE.	IDE	LFIL	ENCE	atch	cal		
£	013766	013766;	01-NOV-1996	01-NOV-1996	01-1	ATRI	HOMO	EUKA	CATARRHINI; HOMINIDAE; HOMO.	Ξ	SEQUENCE FROM N.A.	MEDLINE; 85206210.	SEID	DUBY	Mo]	HYPE	EMBL	EMBL	PROS	PFAM	VASO	SIGNAL	PEPTIDE	PEPTIDE	DISULFID	SEQUENCE	Ouerv Match	Best Local Similarity 100.0%;	Matches	
RESULT		_	_		_	60	10		_			_									•			۔	_	~	One	Bes	Mat	
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GIARDIA INTESTINALIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-WB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LT 5
077443
077443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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        SOR RITARA
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:
ANP.

OVIS ARIES (SHEEP).

EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA; MAMMALIA: EUTHERIA;

ARTIODACTYLA: RUMINANTIA; PECORA; BOVOIDEA: BOVIDAE: CAPRINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                            SEQUENCE FROM N.A.
AITKEN G.D., RAIZIS A.M., GEORGE P.M., ESPINER E.A., CAMERON V.A.;
SUBMITTED (DEC.-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF037465; GZ708659; --
PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
SEQUENCE 152 AA; 16368 MW; D5360BCC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-DELTA H;
MEDLINE: 98037514.
MEDLINE: 98037514.
MITH D.R., DOUCETTE-STAMM L.A., DELOUGHERY C., LEE H.-M., DUBOIS ,
ALDREDGE T., BASHIRAADEH R., BLAKELY D., COOK R., GILBERT K.,
HARRISON D., HOANG L., KEAGLE P., LUMM W., POTHIER B., QIU D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MTH1746.
METHANOBACTERIUM THERMOAUTOTROPHICUM.
ARCHARA: EURYARCHAEOTA; METHANOBACTERIALES; METHANOBACTERIACEAE;
METHANOBACTERIUM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TUPAIA BELANGERI.
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
SCANDENTIA; TUPAIIDAE; TUPAIA.
                                                                                                                                                                                                                                                                                                                                                    Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 155;
                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-HEART;
SCHNEIDEMANN S., MAEGERT H.J., FORSSMANN W.G.;
SUBMITTED (MAR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PARDIGOL A.;
SUBMITTED (MAR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
SUBMITTED (MAR-1996). -
PROSITE: PS00263: NATRIURETIC_PEPTIDE; 1.
PRAM: PF00212: ANP: 1.
SEQUENCE 155 AA: 16860 MW; 77E8CA8B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
CARDIODILATIN, ATRIAL NATRIURETIC PEPTIDE.
                                                                                                                                                                                                                                                                                                                                              Score 101; DB 6; Ler
Pred. No. 1.40e-08;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Match 93.1%; Score 94; DB 6; Le Local Similarity 86.7%; Pred. No. 5.26e-07; les 13; Conservative 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         155 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ź
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01-JAN-1998 (TREMBLREL. 05, LAST SEQ
01-AUG-1998 (TREMBLREL. 07, LAST ANW
CYTOCHROME C-TYPE BIOGENESIS PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 LRAMLAAPRSLRRSS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 LRALLTAPRSLRRSS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [2]
SEQUENCĘ FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LT 4
027778
027778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 029130;
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ID Q29130
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Matches
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        SOSSERVES
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SIKALINE: BY SARCHOLZ.

MEDLINE: 9284022.

HASHIMOTO T., SANCHEZ L.B., SHIRAKURA T., MULLER M., HASEGAWA M.;

"Secondary absence of mitochondria in Giardia lambita and Trichomonas vaginalis revealed by valyl-tRNA synthetase phylogeny.";

DROC NATL. ACAD. SCI. U.S.A. 95:6860-6865(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
ACTINOMYCETALES; CORYNÉBACTERINEAE; MYCOBACTERIACEAE; MYCOBACTERIUM.
                                                                                                                                                                                                                                                                                                                                                                     Gaps
SPADAFORA R., VICARE R., WANG Y., WIERZBOWSKI J., GIBSON R., JIWANI N., CARUSO A., BUSH D., SAFER H., PATWELL D., PRABHAKAR S., MODOGOALL S., SHIMER G., GOYAL A., PIETROVSKI S., CHURCH G.M., DANIELS C.J., MAO J.-I., RICE P., NOLLING J., REEVE J.N.; "Complete genome sequence of Methanobacterium thermoautotrophicum deltah: functional analysis and comparative genomics."; D. BACTERIOL. 179:7135-7155(1997).

EMBL; AEGO0930; G2622078; ...
SEQUENCE 196 AA; 21469 MW; CA13344D CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1218;
                                                                                                                                                                                                                                                                                                 Score 65; DB 1; Length 196;
Pred. No. 5.20e-01;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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1D 006308

AC 0063108

CO 063108

CO 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

CO MYCOBACTERIUM TUBERCULGSIS.

CO BACTERIA, FIRMICUTES, ACTINOBACTERIA, ACTINOBACTERIDAE;

CO C ACTINOMYCETALES, CORYNEBACTERINEAE; MYCOBACTERIDAE;

CO C ACTINOMYCETALES, CORYNEBACTERINEAE; MYCOBACTERIACEAE;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-H37RV;

RA SENTLES S., CHURCHER C.M.;

RA SEQUENCE FROM N.A.

SCORINITED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

RA SERRELL B.G., RAJANDREAM M.A., PARKHILL J.;

RL SUBMITTED (MAY-1996) TC EMBL/GENBANK/DDBJ DATA BANKS.

RN [3]

RP SEQUENCE FROM N.A.

RA SEQUENCE FROM N.A.

RA SUBMITTED (MAY-1996) TC EMBL/GENBANK/DDBJ DATA BANKS.

RN [3]

RP SEQUENCE FROM N.A.
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GENTLES S., CHURCHER C.M.;
SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
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SUBMITTED (MAY-1996) TC EMBL/GENBANK/DDBJ DATA BANKS.
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LAST ANNOTATION UPDATE)
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EMBL, ABO08525. D1029779; -.
AMINOACYL-THAN SYNTHASE.
SEQUENCE 1218 AA. 139225 MW; E98D0361 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 63; DB 5; L
Pred. No. 1.22e+00;
5; Alsmatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1218 AA
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08
08
08
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ilarity 58.3%;
Conservative
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 53.3%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             163 LRRLLRGSRDIRRAS 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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(TREMBLREL.
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1 LRALLTAPRSLRRSS 15
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| LRALLTAPRSLR 12
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MEDLINE; 97251357.

AIBA H., BABA T., FUJITA K., HAYASHI K., INADA T., ISONO K., ITOH T., KASAI H., KASHIMOTO K., KIMORA S., KITARAWA M., KITAGAMA M., MIXELLING K., MIXI T., MAZOBUCHI K., MORI H., MORI T., MOTOMURA K., NAKAMORE S., NAKAMORE Y., NASHIMOTO H., NISHIO Y., OSHIMA T., SAMPEI G., SEKI Y., SIVASUNDARAM S., TAGAMI H., TAKEDOTI Y., TAKEOCHI Y., WADA C., YAMAMOTO Y., HORIUCHI T.; TAKEOOTO K., TAKEOCHI Y., WADA C., YAMAMOTO Y., HORIUCHI T.; COLTESPONDING SEQUENCE OF THE ESCHEZICHIA COLI K-12 genome COLTESPONDING TO THE 28.0-40.1 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BACTERIA; FIRMÍCUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
ACTINOMYCETALES; PSEUDONOCARDINEAE; PSEUDONOCARDIACEAE; AMYCOLATOPSIS.
     Gaps
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                                                                                                                                                                                                                                                                                                                                         ESCHERICHIA COLI.
BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
ESCHERICHIA.
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EMBL: D90819; G1742866; -. PEMBL; AE00019; G1742865; -. PFAM: PF00005; AEC_tran; 1. SEQUENCE 246 AA; 27349 MW; 32F5AC45 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 246;
     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                            02, CREATED)
02, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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KIM C.G., YU I.W., FRYHLE C., HANDA S., FLOSS.H.G.;
J. BIOL. CHEM. 0:0-0(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 60; DB 2; Lo
Pred. No. 4.28e+00;
3; Mismatches 1
     Mismatches
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                                                                                                                                                                                                 PRT;
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01-JUN-1998 (TREMBLREL. 06,
01-JUN-1998 (TREMBLREL. 06,
01-AUG-1998 (TREMBLREL. 07,
KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 30-246 FROM N.A.
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Local Similarity 63.6%;
hes 7; Conservative
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  Conservative
                                               215 LKALAALPKALRRRT 229
                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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1 LRALLTAPESLRRSS 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 97426617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                     LT 9
P76909 PREI
P76909; P76225;
  7;
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052554
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                                                                                          "An integrated map of the genome of the tubercle bacillus, Mycobacterium tuberculosis H37Rv, and comparison with Mycobacterium
                      PHILIPP W.J., POULET S., EIGLMEIER K., PASCOPELLA L.,
BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PSEUDOMONAS GROUP;
PSEUDOMONAS.
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                                                                                                                                                                                                                                                                                         Score 61; DB 2; · Length 215; Pred. No. 2.83e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 61; DB 12; Length 216
Pred. No. 2.83e+00;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                           2; Indels
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YAP W.H., LI X., SOONG T.W., DAVIES J.E.;
SUBMITTED (FEB-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL: U49150; G1854635; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-PAK;
COYNE M.J., GOLDBERG J.B.;
SUBMITTED (JUL-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; UG316; G2226277; --
EMBL; UG316; G2226277; --
EMBL; UG316; G2226277; --
EMBL; UG316; G3226277; --
EMBL; UG3171. Clure transf 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1997 (TREMBLREL. 03, CREATED)
01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
70-KDA HEAT SHOCK PROTEIN (FRAGMENT).
HSP70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .1 8 033426 PRELIMINARY; PRT; 373 AA. 033426; 033426; 01-398 (TREMBLREL. 05, CREATED) 01-3AN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE) 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                            leprae.";
PROC. NATL. ACAD. SCI. U.S.A. 93:3132-3137(1996)
EMBL: 295324; E315475; -...
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.4%; Score 61; DB 2; I 46.7%; Pred. No. 2.83e+00;
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216 216
216 AA; 23489 WW; 106DD33C CRC32;
                                                                                                                                                                                                                                            215 AA; 23102 MW; FD0F1C28 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          373 AA; 42166 MW; 0551B3E1 CRC32;
                                                                                                                                                                                                                                                                                                                                           5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        216 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UNIDENTIFIED SOIL ORGANISM.
UNCLASSIFIED; ENVIRONMENTAL SAMPLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 60.4%;
Local Similarity 58.3%;
nes 7; Conservative
                                                                                                                                                                                                                                                                                         / Match 60.4%;
Local Similarity 53.3%;
nes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         189 LRDGVAAPRPVRRST 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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| LRALLTAPRSLRRSS 15
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2 RALLTAPRSLRR 13
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Best Local Similarity
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SEQUENCE FROM N.A.
96181548
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SEQUENCE 37
                                                                        COLE S.T.;
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NON_TER
SEQUENCE
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P97981;
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Matches
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ULT 14
080398 PRELIMINARY;
080398;
01-NOV-1998 (TREMBLREL. 08, C.
01-NOV-1998 (TREMBLREL. 08, L.
01-NOV-1998 (TREMBLREL. 08, L.
MAP KINASE KINASE 5.
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Best Local Similarity 46.7%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 58.4%;
Local Similarity 40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
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| LRALLTAPRSLRRSS 15
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| LRALLTAPRSLRRSS | 15
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096517
096517;
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ID 08
AC 08
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DT 01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUMAN CYTOMEGALOVIRUS.
VIRUSES; DSDNA VIRUSES, NO RNA STAGE; HERPESVIRIDAE; BETAHERPESVIRINAE;
CYTOMEGALOVIRUS.
                                                                                       FIGURE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-S699;
AUGUST P.R., TANG L., YOON Y.J., NING S., MUELLER R., HUTCHINSON C.R., FLOSS H.G.;
SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF040570; G2792326; -..
SEQUENCE 303 AA; · 30823 MW; FAEA9BDI CRC32;
SEQUENCE 303 AA; · 30823 MW; FAEA9BDI CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHA T.A., TOM E., KEMBLE G.W., DUKE G.M., MOCARSKI E.S., SPAETE R.R., "Human cytomegalovirus clinical isolates carry at least 19 genes not found in laboratory strains.";
J. VIROL. 70:78-83(1996).
EMBL: U33331; G1167937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BRISTOL N2;
MEDLINE; 94150718.
WILSON R., ANDERSON K., BAYNES C., BERKS M.,
WILSON R., AINSCUCH R., ANDERSON K., BAYNES C., BERKS M.,
CRAYCON J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DORBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAMWINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAENORHABDITIS ELEGANS.
EUKARYOTA, METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIBAE; PELODERINAE; CAENORHABDITIS
AUGUST P.R., TANG L., YOON Y.J., NING S., MUELLER R., YU T.W., TAYLOR M., HOFFMANN D., KIM C.G., ZHANG X., HUTCHINSON C.R., FLOSS H.G.;
CHEM. BIOL. 5:0-0(0002).
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                                                                                                                                                                                                                                                                                                Score 60; DB 2; Length 303;
Pred. No. 4.28e+00;
5; Mismatches 2; Indels
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST ANNOTATION UPDATE)
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061790
PRELIMINARY;
061790;
01-AUG-1998 (TREMBLREL. 07, C:
01-AUG-1998 (TREMBLREL. 07, L:
01-NOV-1998 (TREMBLREL. 08, L:
R12E2.11 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TREMBLREL. 01,
01-NOV-1996 (TREMBLREL. 01,
01-NOV-1998 (TREMBLREL. 08,
                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 53.3%;
Matches 8; Conservative
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Best Local Similarity 53.3%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 178 LQALASGPATLRRAS 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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| LRALLTAPRSLRRSS 15
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STRAIN-TOLEDO;
MEDLINE; 96099416.
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Q68404
Q68404;
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EUKARYOTA: VIRIDIPLANTÂE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
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PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN RAALDON W., SMITH A., SONHAMER E., STABLEN R., SILSTON J., THEBRY MEG J., THOMAS K., VAUGHAN K., WATERSTON R., WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.; TAZ Mb of contiguous nucleotide sequence from chromosome III of C. elegans."; NATURE 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i - SIMILARITY: PARTIAL WITH OTHER PHOSPHORIBOSYLTRANSFERASE ALSO INVOLVED IN BIOSYNTHESIS OR SALVAGE OF PURINES OR PYRIMIDINES. EMBL; AF067219; G3150523: P. PROSTER: PS00103; PUR_PYR. P. TRANSFER; 1. TRANSFERASE, GLYCOSYLTRANSFERASE, SEQUENCE 227 AA; 25192 MM; ADIED310 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1997 (TREMBLREL. 02, CREATED)
01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
MAP KINASE KINASE ALPHA PROTEIN KINASE (EC 2.7.1.37)
(PHOSPHORYLASE B KINASE KINASE) (GLYCOGEN SYNTHASE A KINASE)
(HYDROXYALKYL-PROTEIN KINASE) (SERINE(THREONINE) PROTEIN KINASE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 59; DB 5; Length 227; Pred. No. 6.44e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
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                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-BRIGGOL N2;
GOBLA D., SCHEET P.;
SUBMITTED (MAY-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-BRIDO N2;
WARIBSTON R.;
WUBMITTED (MAY-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
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LAST ANNOTATION UPDATE)
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Pred. No. 6.44e+00;
4; Mismatches 4;
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SEQUENCE FROM N.A.
JOUDANNIC S., HAMAL A., KREIS M., HENRY Y.;
PLANT PHYSIOL. 112:1397-1397(1996).
EMBL; YTO7694; ES53927; -.
PFAM: PFO0069; pkinase; 1.
PRANE: 14316; ARAth;2349,mn14316.
TRANSFERASE; PROTEIN KINASE.
SEOUENCE 348 AA; 38329 MW; E9A05E6F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Mismatches
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ANGIOTENSIN/VASOPRESSIN RECEPTOR AIL/AVP.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
              ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUFHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPHRALES; BRASSICACEAE; ARABIDOPSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                   MAO M., ZHANG Q., FU G., HUANG Q., WU J., YU Y., XU S., SHENG J., ZHOU J., WANG Y., CHEN Z.;
ZHOU J., WANG Y., CHEN Z.;
Indentification of genes expressed in human CD34(+) hematopoietic stem/progenitor cells by expressed sequence tags and efficient full-length cDNA cloning.";
FULL -Length CDNA cloning.";
EMBL: ARCAD. SCI. U.S.A. 95:8175-8180(1998).
EMBL: ARCAD. SCI. U.S.A. 95:8175-8180(1998).
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                                                                                                                                                                                                                                                              Length 348;
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Pred. No. 6.44e+00;
5; Mismatches 1; Indels
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LAST ANNOTATION UPDATE)
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Pred. No. 6.44e+00;
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Best Local Similarity 53.8%;
Matches 7; Conservative
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Best Local Similarity 46.7%;
Matches 7; Conservative
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| LRALLTAPRSLRRSS 15
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| LRALLTAPRSLRR 13
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                                                                                                     SEQUENCE FROM N.A.
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Search completed: Wed Jun 16 13:20:44 1999 Job time: 40 secs.

17 41 100.0 25 7 R40563 (Asn136)haNVP(127-151 2.82e+02 196.0 25 7 R40440 (D-Ala138)rANVP(126-13 2.82e+02 20 41 100.0 25 7 R40423 (D-Cys146)haNVP(126-150 2.82e+02 21 41 100.0 25 7 R40423 (D-Ala131)rANVP(126-15 2.82e+02 23 41 100.0 25 7 R40423 (D-Ala131)rANVP(126-13 2.82e+02 24 1 100.0 25 7 R40412 (D-Ala131)rANVP(126-13 2.82e+02 24 1 100.0 25 7 R40412 (D-Ala131)rANVP(126-13 2.82e+02 24 1 100.0 25 7 R40412 (D-Ala131)rANVP(126-13 2.82e+02 24 1 100.0 26 3 R21585 ANVF 416. 2.82e+02 28 41 100.0 26 3 R21585 ANF (3-28) D-ALA(9) P 2.82e+02 29 41 100.0 26 3 R21582 ANF (3-28) D-ALA(9) P 2.82e+02 29 41 100.0 27 2 R62553 (Generic natriuretic peptide 2.82e+02 29 41 100.0 27 2 R62553 (Generic natriuretic peptide 2.82e+02 29 41 100.0 27 2 R62554 (CNP analogue Generic 2.82e+02 29 41 100.0 28 3 R50484 (CNP analogue Generic 2.82e+02 29 41 100.0 28 3 R50484 (CNP analogue Generic 2.82e+02 29 41 100.0 28 3 R50484 (CNP analogue Generic 2.82e+02 29 41 100.0 28 3 R50484 (CNP analogue Generic 2.82e+02 29 41 100.0 28 3 R50484 (CNP analogue Generic 2.82e+02 29 41 100.0 28 3 R50484 (CNP analogue Generic 2.82e+02 29 41 100.0 28 3 R50484 (CNP analogue Generic 2.82e+02 39 41 100.0 28 3 R50484 (CNP analogue Generic 2.82e+02 39 41 100.0 32 (CNP analogue Generic 2.82e+02 39 41 100.0 32 (CNP analogue Generic 3 R50494 (CNP analogue 3	ALIGNMENTS	SUL		region	EP-497368-A 05-AUG-1992 31-JAN-1992		
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nit.			6:part6 7:part7 18:part13 13:part13 18:part23 23:part23 28:part28 33:part33		have a ing printed, n.	Pred. No.	2.82e+02 2.82e+02
computing Research U ty of Edinburgh, U.K ford Molecular Ltd ch, using Smith-Wate	residues	sə	a-geneseg35 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 8:part8 9:part9 10:part10 11:part11 12:part12 11 14:part14 15:part15 16:part16 17:part17 18:part1 19:part19 20:part20 21:part21 22:part22 23:part2 4:part24 45:part25 26:part26 27:part27 28:part2 29:part29 30:part30 31:part31 32:part37 38:part3 34:part34 35:part35 36:part36 37:part39 38:part39	1.977; scale 0.349	predicted by chance to have score of the result being pritotal score distribution.	:S Description	CNP analogue (26). Alpha human atrial na Atrial peptide analog [Arg129][D-Ala131][D-ANVP #38. ANVP #38. ANVP #37. Natriuretic peptide. [Arg129][D-Ala132][D-ANVP #35. Natriuretic peptide. [Arg129][D-Ala132][D-ARg129][D-Ala132][D-ARg129][D-Ala132][D-ARg129][D-Ala131][D-ARg129][D-Ala131][D-ARg129][D-Ala131][D-ARg129][D-ARg139][
	.51 segs, 21266608	Minimum Match 0% Listing first 45 summarie	ipart1 2:part2 3:part i:part8 3:part9 10:par 4:part14 15:part5 10:par 9:part19 20:part20 21 4:part24 25:part25 26 9:part29 30:part35 36 4:part39	Mean 14.664; Variance 41.977;	umber of results or equal to the analysis of the	SUMMARIES	22 35 R29918 22 35 W70089 22 1 P40675 22 7 R40674 23 7 R36974 23 7 R36973 23 7 R40654 23 7 R40654 23 7 R40654 23 7 R40654 23 7 R40654 24 4 P94851 25 7 R40402 25 7 R40456
elease 3. opyright protein wed put not g telease 1. opyright protein wed wed let 0.	170.	••	ଫୁଲ∞ ଲିଲିରିବିଲିଲି ଅ	Меа	No. is greater s derive	% Query re Match	441 1000.0 441 1000.0
MPSrch_pp Run on: Tabular outp Title: Description: Perfect Scor	Searched:	Post-processing	Database:	Statistics:	Pred. score and is	Result No. Scor	

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ALIGNMENTS

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Atrial peptide analogues - are diuretics and hypotensives.
Atrial peptide analogues - are diuretics and hypotensives.

Ala at the 3 position is D-Ala. Tyr22 has an NH2 group attached.

The peptide increases the cyclic GMP produced in assayed cells at considerable greater levels than Atriopeptin III and alpha-hANP,

See also P81568-P81572.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polypeptide cod. - useful as natriuretic, diuretic and/or vasodilator in mammals
Disclosure, Column 52; 45pp; English.
The sequences given in R40387-748 are atrial natriuretic/
vasodilator peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of fluic volume and blood pressure in host organisms. These ANVP fragments may be produced by solid-phase techniques. See also R36937-78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [Arg129][D-Ala132][D-Ser148]haNVP(130-145).
Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
regulation; fluid volume; blood pressure.
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Pred. No. 2.82e+02;
Oraniches 0; Indels
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                                                                                                                  /note="beta-mercaptopropanoic acid Disulphide-bonds 1..17
                                                      Location/Qualiflers
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misc_difference 19
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                                                                                              /label= OTHER
                                                                                                                                                                         26-74N-1988.
09-MAY-1986; 861528.
09-MAY-1986; 105-861528.
(PENI-) Peninsula Labs Inc.
WPI: 88-049653/07.
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WPI; 93-175525/21.
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Best Local Similarity 100.0%;
Matches 5; Conservative
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Local Similarity 100.0%;
nes 5; Conservative
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18-MAY-1993.
09-APR-1984; 602117.
09-APR-1984; US-602117.
01-JUN-1984; US-616488.
      atriopeptin; alpha-hANP
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-MAY-1985; US-766030
05-JUN-1986; US-870795
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Lewicki JA, Scarborou
                                                                        misc_difference 1..1
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This represents a human alpha atrial natriuretic peptide sequence and the invention provides a composition for treating cardiac diseases associated with cardiac hypertrophy. The composition comprises an artive ingredient capable of binding to the peptide receptor of GC-A and promoting production of cGMP. The drug composition may be used clinically to treat cardiac diseases caused by cardiac hypertrophy, including chronic heart failure, ischaemic cardiac diseases and cardiac hypertrophy and teachive substance can bind to the natriuretic peptide receptor of GC-A and promote production of GGMP, effectively preventing cardiac hypertrophy and leading to improvement of the pulmonary blood circulation. The substance does not affect haemodynamic properties,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-0CT-1998 (first entry)
Alpha human atrial natriuretic peptide (alpha-hANP) 2 (residues 7-28).
ANP: atrial natriuretic peptide: cardiac disease; cardiac hypertrophy; chronic heart failure: ischaemic cardiac disease; arrhythmia; cGMP: pulmonary blood circulation; haemodynamic property.
that contain unusual amino acid (non-native type) derivs. would probably exhibit resistance to proteases in the living body (in blood and on the surface of cells) upon admin. In vivo. Therefore, those derivs. even if they have a lower cyclic GMP producing activity than CNP-22 or alpha-hANP, would be characterised by a longer blood half-life than CNP analogs free from unusual amino acids, and, from this viewpoint, too, those derivs. are anticipated to have industrial
                                                                                                                                                                      Cyclic GMP producing activity for CNP analog (26) is 255% increase for 1 microm, compared to 100% for alpha-hANP and 621% for CNP-22 (specific activity as compared to the activity of 1 microm alpha-hANP (2000 fmol/400000 cells), with max. activity being equiv. to the Sequence 22 AA;
                                                                                                                                                                                                                                                                                                                                                                          Gaps
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PB1568 standard: protein; 22 AA.
PB1568:
10-0CT-1990 (first entry)
Atrial peptide analog with diuretic and natriuretic activities
Atrial peptide analog; diuretic; natriuretic; hypotensive activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drug composition comprises natriuretic peptide(s) - for safe treatment of cardiac hypertrophy associated diseases and chronic
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Pred. No. 2.82e+02;
0; Mismatches 0; Indels
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Pred. No. 2.82e+02;
0; Mismatches 0; Indels
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W70089 standard; peptide; 22 AA.
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Best Local Similarity 100.0%;
Matches 5; Conservative
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Matches 5; Conservative
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05-FEB-1997; JP-022594.
(SUNR ) SUNTORY L'ID.
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|NSFRY 5
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28-OCT-1998
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The sequences given in R36937-78 are atrial natriuretic/vasodilator
peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation
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Disclosure; Column 51; 45pp; English.
The sequences given in R40387-748 are atrial natriuretic/
vasodilator peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of fluid volume and blood pressure in host organisms. These ANVP fragments may be produced by solid-phase techniques. See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
regulation; fluid volume; blood pressure.
                                                                                                                                               14-SEP-1993 (first entry)
frag128|D-Alal13||D-Ser147|raNVP(129-145)-NH2.
Human: pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat;
regulation: fluid volume; blood pressure.
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Pred. No. 2.82e+02;
0; Mismatches 0:
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                              T 5
R40674 standard; Protein; 22 AA.
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Best Local Similarity 100.0%;
Matches 5; Conservative
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09-APR-1984; 602117.
09-APR-1984; us-602117.
01-JUN-1984; us-616488.
08-MAY-1985; us-766030.
05-JUN-1986; us-766030.
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08-MAY-1985; US-766030
05-JUN-1986; US-870795
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Lewicki JA, Scarborou
WPI: 93-175525/21.
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09-APR-1984; 602117.
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WPI; 93-175525/21
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                                                                                                        R40674;
14-SEP-1993
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                           RACE SOLL TARGET TO THE SOLUTION TO THE SOL
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The sequences given in R36937-78 are atrial natriuretic/vasodilator peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of fluid volume and blood pressure in host organisms. These ANVP fragments may be produced by solid-phase techniques. See also R40387-749.
                                                                                                                                        Gaps
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regulation; fluid volume; blood pressure.
    These ANVP
                      See also
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Natriuretic peptide.

Noluretic; atrial natriuretic facotr; ANF; hypotensive agent; hypertension; vasodilation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 41; DB 7; Length 23;
Pred. No. 2.82e+02;
0; Mismatches 0; Indels
                                                                                                 Score 41; DB 7; Length 23;
Pred. No. 2.82e+02;
0; Mismatches 0; Indels
of fluid volume and blood pressure in host organisms. fragments may be produced by solid-phase techniques. R40387-749.
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R36973 standard; Protein; 23 AA.
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disulfide_bond 2..18
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20-MAY-1986; CA-509564.
(ADPE) ADV PEPTIDE DEV LTD.
Deghenghi R, Immer HU;
WPI; 87-329003/47.
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Best Local Similarity 100.0%;
Matches 5; Conservative
                                                                                               Query Match
Best Local Similarity 100.0%;
Matches 5; Conservative
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14-SEP-1993 (first entry)
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01-JUN-1984; US-616488
08-MAY-1985; US-766030
05-JUN-1986; US-870795
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Lewicki JA, Scarborou
WPI; 93-175525/21.
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                                                          23 AA;
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Modified_site
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NSFRY 5
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25-NOV-1987
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vasodilator in mammals
Disclosure; Column 11, 45pp; English.
The sequences given in R36937-78 are atrial natriuretic/vasodilator
peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation
of filld volume and blood pressure in host organisms. These ANVP
fragments may be produced by solid-phase techniques. See also
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The sequences given in R40387-748 are atrial natriuretic/vasodlator peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of fluid volume and blood pressure in host organisms. These ANVP fragments may be produced by solid-phase techniques. See also R36937-78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-SEP-1993 (first entry)
[Arg128][D-Ala11][D-Ala142]rANVP(129-150).
Human: pre-pro; arrial natriuretic/vasodilator peptide; ANVP; rat;
regulation; fluid volume; blood pressure.
                                                                 18-MAY-1993.
09-ARR-1984, G62117.
09-ARR-1984, US-602117.
01-JUN-1984, US-616488.
08-MAY-1985, US-766030.
05-JUN-1986; US-870795.
(SCIO-) SCIOS NOVA INC.
LEWICK! JA, Scarborough RM;
WPI; 93-175525/21.
New polypeptide cpd. - useful as natriuretic, diuretic and/or
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                                                                                                                                                                                                                                                                                                                                                                                                 Score 41; DB 7; Length 23;
Pred. No. 2.82e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                               DB 7; Length 23;
                                       "D-form residue"
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R40654 standard; Protein; 23 AA.
R40654;
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Lewicki JA, Scarborough RM;
WPI; 93-175525/21.
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Best Local Similarity 100,0%;
Matches 5; Conservative
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Best Local Similarity 100:0%;
Matches 5; Conservative
                                       /note-
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08-MAY-1985; US-766030
05-JUN-1986; US-870795
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   2..18
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                                                                                                                                                                                                                                                                                                                                                                23 AA;
   disulfide_bond
misc_difference
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09-APR-1984;
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Disclosure; Column 50: 45pp; English.
The sequences given in R4038+7.
These squences given in R4038+7.
These for regulation of fluid volume and blood pressure in host organisms.
These ANVP fragments may be produced by solid-phase techniques. See
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                                                                                                                                                                                                                                             Gaps
New synthetic natriuretic peptide(s) - contg. 23 amino acid(s) and having eg diuretic, vaso-relaxant and antihypertensive activities.
                                                 Claim 5: Page 16: 16pp: English.

The peptide shows dissociation of diuretic and natriuretic effects from undesirable vasorelaxant effects on the heart rate, and duration of action is longer than for known natriuretic peptides. It is prepd. by solid phase synthesis. The C-terminal bea an OH or NH2 yp.
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Synthetic. Location/Onslificer
                                                                                                                                                                                                                                                                                                                                                                                                                               (Arg129)(D-Ala132)(D-Cysi46)hANVP(130-151).
Human: pre-pro: atrial natriuretic/vasodilator peptide: ANVP: rat:
regulation; fluid volume: blood pressure.
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                                                                                                                                                                                                     Score 41; DB 2; Length 23;
Pred. No. 2.82e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41; DB 7; Length 23;
Pred. No. 2.82e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note- "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "D-form residue"
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                                                                                                                                                                                                                                                                                                                                                                T 9
R40663 standard; Protein; 23 AA.
R40663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R36971 standard; Protein; 23 AA. R36971;
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Best Local Similarity 100.0%;
Matches 5; Conservative
                                                                                                                                                                                                       Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 14-SEP-1993 (first entry)
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ANVP #35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-602117.
US-616488.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-MAY-1985; US-766030
05-JUN-1986; US-870795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SCIO-) SCIOS NOVA INC
Lewicki JA, Scarborou
WPI; 93-175525/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      602117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_difference 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  also R36937-78
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NSFRY 5
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                                                                                                                                                                                                                                                                                              US5212286-A.
                                                                                                                                                                         Seguence
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vasodilator in mammals
Disclosure; Column 54; 45pp; English.
The sequences given in R40387-748 are atrial natriuretic/
vasodilator peptide (ANVP) cDNAs. These ANVP fragments may be used for regulation of fluid volume and blood pressure in host organisms.
These ANVP fragments may be produced by solid-phase techniques. See also R36937-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diuretic compsn. contg. atrial peptide -
in from for nasal admin. pref. in aq. soln.
Claim 1; Page 8; 10pp; English.
Derivatives of the diuretic peptide may have one or both C-terminal
residues and up to four N-terminal residues absent.
Sequence 24 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [Ser136]JANVP(127-151).

Human; pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat; regulation; fluid volume; blood pressure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polypeptide cpd. - useful as natriuretic, diuretic and/or
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                                                                                                                                                                                                                                                                       10.52P-1990 (first entry)
Intranasally effective diuretic atrial peptide.
Diuretic; atrial peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 41; DB 1; Lv
Pred. No. 2.82e+02;
0; Mismatches 0
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Pred. No. 2.82e+02;
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label=May be Ile or Met
                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
3..19
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R04102 standard; peptide; 24 AA.
R04102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R40702 standard; Protein; 25 AA. R40702;
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01-JUN-1984; US-602117.
08-MAY-1985; US-766030.
05-JUN-1986; US-870795.
(SCIO-) SCIOS NOVA INC.
Lewicki JA, Scarborough RM;
WPI; 93-175522/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%;
Matches 5; Conservative
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Best Local Similarity 100.0%;
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5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9-MAY-1986; 508837.
10-MAY-1985; US-732781.
(MONS) Monsanto Co.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Klopf LL, Hecht RI;
WPI; 90-124666/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_difference
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| NSFRY 5
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                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
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Matches
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Example: Page 15, 24pp; German.
P93041,P94848-P94853; P93098-P93100 are examples of the generic formula for peptides of the invention. They have diuretic, natriuretic and vasodilatory activity, and also immunomodulatory activity. They may also be used to treat renal insufficiency and to protect the kidneys against renal toxins, e.g. cyclosporin during kidney transplantation, and for treating glaucoma and/or reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alpha-hANP peptide analogues -
are hypotensives and natriuretics.
Claim 1, page 32; 33pp; English.
Peptides can be used as a therapeutic drug for hypertension, a diuretic, for cardiac and cerebral circulatory diseases and as muscle relaxant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                              05-DEC-1990 (first entry)
Alpha-human Atrial Natriuretic Peptide (hANP) analogue #3.
alpha-human Atrial Natriuretic Peptide analogue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAR-1992 (first entry)
Sequence of atrial natriuretic factor (ANF) analogue
Diuretic; natriuretic; vasodilator; immunomodulator.
Ney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41; DB 1; I
Pred. No. 2.82e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41; DB 4; I
Pred. No. 2.82e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (FARH ) HOECHST AG.
Breipohl G, Knolle J, Konig W, Hropot M;
WPI; 89-016929/03.
                                                                                                                                                                                                                                                                          Key Location/Qualifiers
disulphide_bond 2..18
/note="intramolecular"
                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1988.
29-SEP-1987; 308586.
29-SEP-1986; JP-231429.
(TAKE) Takeda Chemical Ind KK.
Fujino M, Wakimasu M, Nishikawa K.;
WPI; 88-149016/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P94851 standard; peptide; 24 AA.
P94851;
                                                                      P82984 standard; protein; 23 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Tyr(Me)
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Best Local Similarity 100.0%;
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Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  See also P82684 and P82983
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09-JUL-1988; 111011.
16-JUL-1987; DE-723551.
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24 AA;
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1 NSFRY 5
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Matches

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Gaps

5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches g &

Search completed: Wed Jun 16 13:22:58 1999 Job time : 16 secs.

US-09-027-777B-3.rai

24 41 100.0 27 4 5202239-5 25 41 100.0 28 4 5204327-1 28 41 100.0 28 4 5204327-3 28 41 100.0 28 4 5404327-3 29 41 100.0 28 4 5461142-1 29 41 100.0 28 1 5469751-2 31 41 100.0 28 1 05-08-451-3 32 41 100.0 28 1 05-08-451-3 34 41 100.0 28 1 05-08-451-3 35 41 100.0 28 1 05-08-451-3 36 41 100.0 28 1 05-08-451-3 37 41 100.0 28 1 05-08-451-3 38 41 100.0 28 1 05-08-451-3 39 41 100.0 124 4 5202239-1 42 41 100.0 136 4 5512286-4 43 41 100.0 151 4 5212286-6 45 41 100.0 151 4 5212286-6	ALIGNMENTS RESULT 1 ID 5212286-22 STANDARD; PRT; 5 A XX AC XXXXXX	XX DT 01-JAN-1900 XX DE Patent No. 5212286. XX CC Patent No. 5212286	NO. 5212286 TO. 5212286 TLC OF INVERTION: ATR E COMPUNDS MBER OF SEQUENCES: 68 REENT APPLICATION DAT APPLICATION NUMBER: TILING DATE: 05-JUN-1 IOR APPLICATION NUMBER: FILLING DATE: 08-MAY-1 RILLING DATE: 08-MAY-1 RILLING DATE: 08-MAY-1	CC FILING DATE: 09-APR-1984 CC APPLICATION NUMBER: 616,488 CC FILING DATE: 01-UN-1984 CC SEQ ID NO:22: CC LENGTH: 5 SQ SEQUENCE 5 AA; 686 MW; 180 CN; Query Match Best Local Similarity 100.0%; Score 41; 1 Matches 5; Conservative 0; Mismatch Db 1 NSFRY 5	RESULT 2 ID US-07-828-450-26 STANDARD; PRT; XX AC XXXXX XX DT XX DT XX DE Sequence 26, Application US/07828450 XX CC Sequence 26, Application US/07828450
	Title: >US-09-027-777B.pep Description: (1-5) from US09027777B.pep Perfect Score: 1 NSFRY 5 Scoring table: PAM 150 Gap 15	d: ocessing:	se: Lics: red. No score gre and is de	Querry Querry Querry Querry 100.0 5 4 5212286-22 100.0 22 1 US-07-828- Patent No. 5212286. 100.0 22 1 US-07-828- Sequence 27, Applicati 100.0 23 4 5212286-39 100.0 23 4 5212286-39 Patent No. 5212286. 1 100.0 23 4 5212286-37 Patent No. 5212286. 1 100.0 23 4 5212286-37 Patent No. 5212286. 1 100.0 23 4 5212286-47 Patent No. 5212286. 1 100.0 23 4 5212286-45 Patent No. 5212286. 1 100.0 23 4 5212286-45 Patent No. 5212286. 1 100.0 23 4 5212286-45 Patent No. 5212286. 1 100.0 24 5212286-45 Patent No. 5212286. 1 100.0 25 4 5212286-55 Patent No. 5212286.	41 100.0 25 4 5212286-49 Patent No. 5212286. 1.4 1 100.0 25 4 5212286-32 Patent No. 5212286. 1.4 1 100.0 25 4 5212286-32 Patent No. 5212286. 1.4 1 100.0 25 4 5212286-36 Patent No. 5212286. 1.4 1 100.0 25 4 5212286-31 Patent No. 5212286. 1.4 1 100.0 25 4 5212286-37 Patent No. 5212286. 1.4 1 100.0 25 4 5212286-37 Patent No. 5212286. 1.4 1 100.0 25 4 5212286-35 Patent No. 5212286. 1.4 1 100.0 25 4 5212286-35 Patent No. 5212286. 1.4 1 100.0 25 4 5212286-35 Patent No. 5212286. 1.4 1 100.0 25 4 5212286-35 Patent No. 5212286. 1.4 1 100.0 25 4 5212286-35 Patent No. 5212286. 1.4 1 100.0 27 4 5212286-36 Patent No. 5212286. 1.4 1 100.0 27 4 5212286-36 Patent No. 5212286. 1.4 1 100.0 27 4 5212286-36 Patent No. 5212286. 1.4 1 100.0 27 4 5212286-36 Patent No. 5212286. 1.4 1 100.0 27 4 5212286-36 Patent No. 5212286. 1.4 1 100.0 27 4 5212286-36 Patent No. 5212286. 1.4 1 100.0 27 4 5212286-36 Patent No. 5212286. 1.4 1 100.0 27 4 5212286-36 Patent No. 5212286. 1.4 1 100.0 20 4 5212286-36 Paten

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						ALIGNMENTS			
RES	RESULT 1 ID 5212286	-2	. 2	STANDARD;		PRT; 5	AA.		
X Y X	xxxxx	×							
613	01-JA	-JAN-1900	0						
E X	Patent	t No.	. 5212286	86.					
×888888888888888888888	Patent N APPL TITL PEPTIDE CURR CURR FII PRIO PRIO FII SEQ ID N	nt No. 52 APPLICANT TITLE OF TIDE COMPU NUMBER OF CURRENT A APPLICA FILING	NO. 521228 PLICANT: LE TIE OF INVE E COMPUNDS MBER OF SEO RRENT APPLICATION RAPPLICATION APPLICATION FILING DATE APPLICATION FILING DATE APPLICATION FILING DATE RIGHT OF SEO RELING DATE	nt NO. 5212286 APPLICANT: LEWICKI, JOHN TITLE OF INVENTION: ATRIA IDE COMPUNDS CURRENT APPLICATION NAMER: US FILING DATE: 05-JUN-198 PRIOR APPLICATION NUMBER: 766 FILING DATE: 08-MAY-198 APPLICATION NUMBER: 616 FILING DATE: 09-APR-198 APPLICATION NUMBER: 616 FILING DATE: 01-JUN-198 APPLICATION NUMBER: 616 FILING DATE: 01-JUN-198 ID NO:22: LENGRIH: 5 LENGRIH: 5 LENGRIH: 5 LENGRIH: 5 FARE MAY-180	JOHN ATRIA 68 68 68 15 DATA: 11 TA: 12 TA: 13 TA: 16 TA: 17 TA: 18 TA: 1	4.1 0,0 0,1.4.4 X	SCARBOROUGH, ROBERT M. NATRIURETIC/VASODILATOR 7/870,795 30 17 88		
Оща	Query Ma Best Loc Matches	/ Match Local Si nes 5	Similarity 5; Conse	100.0% arity 100.0% Conservative	ال معاددة د	Score 41; DB 4 Pred. No. 1.48e 0; Mismatches	DB 4; Length 5; 1.48e+02; tches 0; Indels 0;	Gaps (ő
g &	е е	NSFRY NSFRY	s s						
RES XX XX	RESULT 2 ID US-07- XX AX AC XXXXXX	828	-450-26	-	STANDARD	PRT	, 22 AA.		
X DX DX	Sequence		26, App]	lication	ns,	Application US/07828450			

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COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/828,450
FILLING DATE: 19920131
CLASSIFICATION: 530
ATTONEY/AGPANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M. TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41; DB 4; L. Pred. No. 1.48e+02; 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41; DB 1; L
Pred. No. 1.48e+02;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                          26,581
ER: 9437/94133
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APPLICATION NUMBER: US/07/870,795
FILING DATE: 05-UN-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 766,030
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TELEX: 6714627 CUSH
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
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ENCE 22 AA; 2369 MW; 2338 CN;
                                                                                                                                                                                                                                                          CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WAJEON T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: 943
TELEPOMNUNICATION INFORMATION:
TELEPHAN: 202-861-3067
TELEPHAN: 202-822-0944
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APPLICATION NUMBER: 616,488
FILING DATE: 01-JUN-1984
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                      STATE: D.C.
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d.
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Local Similarity 100.0%;
hes 5; Conservative
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Best Local Similarity 100.0%;
Matches 5; Conservative
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APPLICATION NUMBER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
WASHINGTON
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STRANDEDNESS: SI
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Best Local S:
Matches
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APPLICANT: FURUYA, MAYUMI
APPLICANT: FURUYA, MAYUMI
ATTLE OF INVENTION: CNP ANALOG PEPTIDES AND THEIR USE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHWAN, DARBY & CUSHWAN
STREET: 1625 L STREET, N.W.
                                                                                                  APPLICANT: FURUYA, MAYUMI
APPLICANT: MATSUO, HISAYUKI
TITLE OF INVENTION: CNP ANALOG PEPTIDES AND THEIR USE
CORRESPONDENCE : 42
CORRESPONDENCE ADDRESS:
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Pred. No. 1.48e+02;
                                                                                                                                                     CITY: WASHINGTON STATE: D.C. COUNTRY COUNTRY.
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ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
--wentTER: IBM PC compatible
--wentTER: "wentRy PC-DOS/MS-DOS
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APPLICANT: TANAKA, SHOJI
APPLICANT: MINAMITAKE, YOSHIHARU
                                                           MINAMITAKE, YOSHIHARU
KITAJIMA, YASUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 27, Application US/07828450
Patent No. 5434133
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NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: 943:
TELECHMUNICATION INFORMATION:
TELECHONE: 202-813067
TELEFAX: 202-822-0944
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22 AA; 2369 MW; 2338 CN;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
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APPLICATION NUMBER: US
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Best Local Similarity 100.0%;
Matches 5; Conservative
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CLASSIFICATION: 530
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Patent No. 5434133
GENERAL INFORMATE
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ID US-07-828-450-27
                                         APPLICANT:
APPLICANT:
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                                                                                       APPLICANT
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Pred. No. 1.48e+02;
0; Mismatches 0; Indels
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Pred. No. 1.48e+02;
0; Mismatches 0; Indels
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APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
PEPTIDE COMPUNDS
NUMBER OF SEQUENCES: 68
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/870,795
FILING DATE: 05-JUM-1986
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                        APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M. TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR PEPTIDE COMPUNDS
                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/870,795
FILING DATE: 05-70N-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 766,030
FILING DATE: 08-MAY-1985
APPLICATION NUMBER: 602,117
FILING DATE: 09-APR-1984
APPLICATION NUMBER: 616,488
FILING DATE: 01-JUN-1984
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FILING DATE: 08-MAY-1985
APPLICATION NUMBER: 602,117
FILING DATE: 09-APR-1984
APPLICATION NUMBER: 616,488
FILING DATE: 01-JUN-1984
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SEQUENCE 25 AA; 2768 MW; 3233 CN;
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25 AA; 2754 MW; 3345 CN;
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Best Local Similarity 100.0%;
Matches 5; Conservative
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Best Local Similarity 100.0%;
Matches 5; Conservative
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ID 52
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Pred. No. 1.48e+02;
0; Mismatches 0; Indels
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Pred. No. 1.48e+02;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/870,795
FILING DATE: 05-JUN-1986
FILING DATE: 08-MAY-1985
APPLICATION NUMBER: 766,030
FILING DATE: 08-MAY-1985
APPLICATION NUMBER: 602,117
FILING DATE: 09-APR-1984
APPLICATION NUMBER: 616,488
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/810,795
FILING DATE: 05-JUN-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 766,030
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CE 25 AA; 2772 MW; 3366 CN;
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SEQUENCE 25 AA; 2768 MW; 3310 CN;
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APPLICATION NUMBER: 602,117
FILING DATE: 09-APR-1984
APPLICATION NUMBER: 616,488
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Best Local Similarity 100.0%;
Matches 5; Conservative
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Best Local Similarity 100.0%;
Matches 5; Conservative
                                                                        STANDARD;
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5212286-39
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ZIP: 20005-3315
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                                                          us-08-257-446-5
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APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M.
TILLO OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
PEPTIDE COMPUNDS

NUMBER OF SEQUENCES: 68

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/870,795

FILING DATE: 05-UN-1986

PRIOR APPLICATION DATE: 66-300

FILING DATE: 08-MAY-1985

APPLICATION NUMBER: 766,300

FILING DATE: 09-APR-1986

APPLICATION NUMBER: 602,117

FILING DATE: 09-APR-1984

APPLICATION NUMBER: 616,488
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Pred. No. 1.48e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                  Length 23;
                                                                                                                                            ant No. 5212286
APPLICANT: LEWICKI, JOHN A.;SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
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Pred. No. 1.48e+02;
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NUMBER OF SEQUENCES: 68

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/870,795

FILING DATE: 05-JUN-1986

APPLICATION NUMBER: 766,330

FILING DATE: 08-MAY-1985

APPLICATION NUMBER: 602,117

FILING DATE: 09-APR 1984

APPLICATION NUMBER: 616,488

FILING DATE: 01-JUN-1984
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NCE 25 AA; 2768 MW; 3261 CN;
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ICE 25 AA; 2768 MW; 3317 CN;
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SEQ ID NO:44:
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Best Local Similarity 100.0%;
Matches 5; Conservative
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Best Local Similarity 100.0%;
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                                                                                                                           Patent No. 5212286.
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19 NSFRY 23
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            1 NSFRY 5
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1 NSFRY 5
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5212286-44
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ID 5212286-45
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TITLE OF INVENTION: The Synthesis of Peptide
TITLE OF INVENTION: Aminoalkylamides and Peptide Hydrazides by the Solid Ph
TITLE OF INVENTION: Method
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CIT: Washingtor.
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Pred. No. 1.48e+02;
0; Mismatches 0; Indels
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24 AA.
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APPLICATION NUMBER: US/08/257,446
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CLASSIFICATION: 530
PRIOR APPLICATION 530
PRIOR APPLICATION CATA:
APPLICATION NUMBER: US 783,335
FILING DATE: 28-0CT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lindeman, Jeffrey A.
REGISTRATION NUMBER: 34,658
REBERBRENG/POCKET NUMBER: 02481-05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-208-4000
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SISTEM: PC-DOS/MS-DOS
                                                                                                                                                                                   Sequence 5, Application US/08257446 Patent No. 5565606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
JENCE 24 AA; 2552 MW; 2660 CN;
                                                                                                                                         Sequence 5, Application US/08257446
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APPLICANT: Knolle, Jochen
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STANDARD;
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SEQUENCE CHARACTERISTIC
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MEDIUM TYPE: Floppy
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Local Similarity 100.0%;
nes 5; Conservative
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                                                                            APPLICATION TEMPORION ATRIAL NATRIURETIC/VASODILATOR PEPTIDE COFFINE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR PEPTIDE COMPUNDS

NUMBER OF SEQUENCES: 68
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/870,795
FILING DATE: 05-JUN-1986
APPLICATION NUMBER: 766,030
FILING DATE: 08-MAY-1985
APPLICATION NUMBER: 602,117
FILING DATE: 09-APR-1984
FILING DATE: 01-JUN-1984
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Pred. No. 1.48e+02;
0; Mismatches 0; Indels
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APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M.
TILLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
PEPPIDE COMPUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41; DB 4; L4
Pred. No. 1.48e+02;
0; Mismatches 0
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ICE 27 AA; 2942 MW; 3718 CN;
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APPLICATION NUMBER: 766,030
FILING DATE: 08-MAY-1985
APPLICATION NUMBER: 602,117
FILING DATE: 09-APR-1984
APPLICATION NUMBER: 616,488
FILING DATE: 01-JUN-1984
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ICE 27 AA; 2942 MW; 3774 CN;
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CURRENT APPLICATION DATA:
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Best Local Similarity 100.0%;
Matches 5; Conservative
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Best Local Similarity 100.0%;
Matches 5; Conservative
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                                          Patent No. 5212286

APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M. TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR COMPUNDS
NUMBER OF SEQUENCES: 68
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/870,795
C FILING DATE: 05-JUN-1986
C PRIOR APPLICATION NUMBER: 766,330
C FILING DATE: 08-MAY-1985
C FILING DATE: 08-MAY-1985
C FILING DATE: 09-APR-1984
C FILING DATE: 09-APR-1984
C APPLICATION NUMBER: 602,117
FILING DATE: 09-APR-1984
C APPLICATION NUMBER: 616,488
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/870,795
FILING DATE: 05-JUN-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 766,030
FILING DATE: 08-MAY-1985
APPLICATION NUMBER: 602,117
FILING DATE: 09-APR-1984
APPLICATION NUMBER: 616,488
FILING DATE: 01-JUN-1984
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ICE 27 AA; 3001 MW; 3736 CN;
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SEQ ID NO:55:
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Matches 5; Conservative
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University'of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algor thm MPsrch_pp

Wed Jun 16 13:23:15 1999; MasPar time 2.89 Seconds 69.204 Million cell updates/se Run on:

Tabular output not generated.

>US-09-027-777B-3 (1-5) from US09027777B.pep 41 1 NSFRY 5 Description: Perfect Score: Sequence: 122810 segs, 40068593 residues Searched:

PAM 150 Gap 15

Scoring table:

Post-processing: Minimum Match 0% Listing first 45 summaries

pir60 1:pir1 2:pir2 3:pir3 4:pir4 Database:

Mean 20.516; Variance 23.884; scale 0.859 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	4.81e+01	4.81e+01	4.81e+01	4.81e+01	4.81e+01	4.81e+01	4.81e+01	4.81e+01	4.81e+01	4.81e+01	4.81e+01	4.81e+01	4.81e+01	4.81e+01	4.81e+01	4.81e+01	4.81e+01	1.21e+02	1.21e+02	1.21e+02	1.21e+02	1.21e+02	1.21e+02
Description P1	hypothetical protein	atrial natriuretic pe 4	ribosomal protein L28 4	ribosomal protein L28	ribosomal protein L28 4	atrial natriuretic pe 4	atrial natriuretic pe	natriuretic peptide A 4	atrial natriuretic fa 4	atrial natriuretic pe 4	atrial natriuretic pe	atrial natriuretic pe	atrial natriuretic pe	hypothetical natriure	nypothetical protein	formate C-acetyltrans	formate C-acetyltrans 4	hypothetical protein . 1	nypothetical protein.		ribonucleoside-diphos	ADP-L-glycero-D-manno	hypothetical protein
ID Desc		S14872 atr		R5RT28 rib	148738 rib	AWDG atr	S13107 atr	AWHU nat	AWRT atr	AWBO atr	AWMS atr	S14873 atr	AWRB atr	155480 hyp	r00602 hyp					_		G70330 ADP	н64082 hyp
DB 1	7	~	7	ד	7	7	7	7	1	7	7	~	7	4	2	7	~	2	7	7	7	~	7
Length D	110	128	137	137	137	149	150	151	152	152	152	153	153	161	635	740	. 746	102	107	230	240	310	315
Suery Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	95.1	95.1	95.1	95.1	95.1	95.1
Score	41	41	4.1	4.1	4.1	4.1	4.1	4.1	41	4.1	4.1	41	4.1	4.1	41	4.1	41	39	39	39	39	39	39
Result No.	-	7	6	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23

\$14872 #type fragment atrial natriuretic peptide precursor - guinea pig (fragment) #formal_name Cavia porcellus #common_name guinea pig 20-Feb-1995 #sequence_revision 30-Jan-1998 #text_change

TITLE ORGANISM DATE

RESULT ENTRY

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Gaps

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1-98 99-128 105-121

SUMMARY

Matches

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ACCESSIONS REFERENCE

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ructure of dog and rabbit precursors of atrial natriuretic polypeptides deduced from nucleotide sequence of cloned
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #formal_name Mus musculus #common_name house mouse 02.Jul-1996 #sequence_revision 02-Jul-1996 #text_change 148738
                                                                                                                                                                                             *product ribosomal protein L28 *status experimental
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ANP: atrial natriuretic polypeptide
#formal_name Canis lupus familiaris #common_name dog
31-Mar-1998 #sequence_revision 31-Mar-1998 #text_change
                                                                                                                                                                                                                  #label MAT
#length 137 #molecular-weight 15849 #checksum 7501
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Blochem. Blophys. Res. Commun. (1985) 132:892-899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Burke, P.S.; Llum, E.; Lln, C.S.; Wolgemuth, D.J. Gene (1994) 142:135-316
Sequence and expression of a CDNA encoding the mo homologue of the rat ribosomal protein L28.
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##moleute_type mRNA.
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##cross-references EMBL:X74856; NID:9488834; PID:9488835
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                  ##molecule_type mRNA
##residues 1-137 ##label WOO
##cross-references EMBL:X52619; NID:g57112; PID:g57113
                                                                        *superfamily rat ribosomal protein L28 #length 137 #molecular-weight 15733
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Best Local Similarity 100.0%;
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##molecule_type mRNA
S13072
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Blophys. Acta (1990) 1150:69-73
The primary structure of rat ribosomal proteins: the amino acid sequences of L27a and L28 and corrections in the
                                                                                                                                                                                                                                                                   #domain signal sequence #status predicted #label SIG\
#product atrial natriuretic peptide #status predicted #label MAT\
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#formal_name Rattus norvegicus #common_name Norway rat
30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ribosomal protein L28 - human
#formal_name Homo sapiens #common_name man
28-oct-1995 #sequence_revision 03-Nov-1995 #text_change
25-Mar-1998
                                                       Maegert, H.J.; Hanke, M.; Schmeding, G.; Teuteberg, K.; Schulz-Knappe, P.; Forssmann, W.G. submitted to the EMBL Data Library, March 1991 514872
                                                                                                                                                                                                                  *superfamily natriuretic peptide A precursor atrium; diuretic; hormone; natriuretic; osmoregulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #authors Frigerio, J.M.; Dagorn, J.C.; Iovanna, J.L. #journal Biochim. Biophys. Acta (1995) 1262:64-68 #title Cloning, sequencing and expression of the L5, L21, L S5, S9, S10 and S29 human ribosomal protein mRNAs.
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Pred. No. 4.81e+01;
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Pred. No. 4.81e+01;
0; Mismatches 0; Indels
                                                                                                                                   ##molecule_type mRNA
##residues 1-128 ##label MAE
##erross references EMBL.X58502; NID:949544
##experimental_source heart atria; adult
                                                                                                                                                                                                                                                                                                                                     #disulfide_bonds #status predicted
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FICATION #superfamily rat ribosomal protein L28
(Y #Hength 137 #molecular-weight 15761
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S13072; A30448
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20-Mar-1998
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##molecule_type mRNA
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S14872
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SUMMARY
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REFERENCE #authors

ACCESSIONS

RESULT ENTRY TITLE ORGANISM DATE

mouse

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#authors #journal #title

ACCESSIONS REFERENCE

TITLE ORGANISM DATE

RESULT

셤 ò S.; Drouin,

122-149 128-144

SUMMARY

1-23 24-149

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prepronatriodilatin (PND)
atrial alpha natriuretic peptide (ANP); cardiodilatin (atrial
gamma natriuretic factor)
farmal name Homo sapiens #common_name man
15-Nov-1984 #sequence_revision 15-Nov-1984 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #journal Blochem. Biophys. Res. Commun. (1984) 118:131-139
#title Purification and complete amino acid sequence of alpha-human atrial natriuretic polypeptide (alpha-hANP).
#cross-references MUID:84128019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nakayama, K.; Ohkubo, H.; Hirose, T.; Inayama, S.; Nakanishi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1-151, 'RR' ##label NE2 allelic variant with UGA termination codon replaced by
                                              factor; atrial natriuretic protein;
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Cikawa, S.; Imai, M.; Ueno, A.; Tanaka, S.; Noguchi, T.;
Nakazato, H.; Rangawa, K.; Fukuda, A.; Matsuo, H.
Nature (1984) 309:724-726
Cloning and sequence analysis of cDNA encoding a precursor for human atrial natriuretic polypeptide.
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I39458; I39459; I39460; I37167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science (1984) 226:1206-1209
Nucleotide sequences of the human and mouse atrial
                                                                                                                                                                                                                                                                                                       Nemer, M.; Chamberland, M.; Sirois, D.; Argentin,
J.; Dixon, R.A.F.; Zivin, R.A.; Condra, J.H.
Nature (1984) 312:654-656
Gene structure of human cardiac hormone precursor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vanneste, Y.; Michel, A.; Deschodt-Lanckman, M.
Eur. J. Biochem. (1991) 196:281-286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##molecule_type_mRNA
##residues 1-151 ##label OIK
##cross-references GB:K02043; NID:9178629; PID:9178630
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##cross-references GB:M30262; NID:g180181; PID:g180182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##residues 1-151 ##label NEM
##cross-references GB:X01470; NID:928687; PID:9825625
                  natriuretic peptide A precursor - human
ANF, atrial natriuretic factor; atrial
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##cross-references GB:K02043
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158054
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#cross-references MUID:85061626
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#accession I58054
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##residues 1-15
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Nucleic Acids Res. (1990) 18:6704
Nucleotide sequence of a porcine prepro atrial natriuretic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            $13107  #type complete
atrial natriuretic peptide precursor - pig
alpha atrial natriuretic peptide; gamma atrial natriuretic
factor (cardiodilatin)
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#product gamma atrial natriuretic factor #status
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#product alpha atrial natriuretic peptide #status
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Anat. Embryol. (1933) 168:307-313
The right auricle of the heart is an endocrine organ.
Cardiodilatin as a peptide hormone candidate.
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##residues 25-54 ##label FOR
FRICATION #superfamily natriuretic peptide A precursor
tDS atrium; diuretic; hormone; natriuretic; osmoregulation
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predicted #label ANP\
##residues 1-149 ##label OIK
##Cross-references GB:M12045; NID:g163900; PID:g163901
CLASSIFICATION #superfamily natriuretic peptide A precursor
KEYWORDS atrium; diuretic; hormone; natriuretic; osmoregulation
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Homcy, C.J.; Duby, A.D.; Choi, E.; Graham, R.M.; Seidman,
                                                                                                                                                                                                                                                                                                                                                                                                               *authors Maki, M.; Parmentier, M.; Inagami, T. adjournal Blochem. Blochys. Res. Commun. (1984) 125:797-802 #1411e Cloning of genomic DNA for human atrial natriuretic factor. #cross-references WUID:85096983
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*title Hydrclysis of intact and Cys-Phe-cleaved human atrial
natriuretic peptide in vitro by human tissue kallikrein.
*cross-references MUID:91176998
*accession S14097
                                                                     *authors Zivin, R.A.; Condra, J.H.; Dixon, R.A.; Seidah, N.G.; Chretien, M.; Nemer, M.; Chamberland, M.; Drouin, J. *journal Proc. Natl. Acad. Sci. U.S.A. (1984) 81:6325-6329 Molecular cloning and characterization of DNA sequences encoding rat and human atrial natriuretic factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypertension (1985) 7:31-34
Molecular studies of the atrial natriuretic factor gene.
139460
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Nature (1984) 312.656-658
Nucleotide sequence of the gene encoding human atrial natriuretic factor precursor.
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*product cardiodilantin *status predicted #label C
*product atrial alpha natriuretic peptide *status
experimental *label ANP\
#disulfide_bonds *status experimental
#th 151 #molecular-weight 16395 *checksum 3644
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*superfamily natriuretic peptide A precursor
atrium; diuretic; hormone; natriuretic; osmoregulation
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Pred. No. 4.81e+01;
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##cross-references GB:K02044; NID:9178631; PID:9178632
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##cross-references GB:K02399; NID:g178633; PID:g178634
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Atlas, S.A.; Kleinert, H.D.; Camargo, M.J.; Januszewicz, A.; Sealey, J.E.; Laragh, J.H.; Schilling, J.W.; Lewicki, J.A.; Johnson, L.K.; Maack, T.
Nature (1984) 309:717-719
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                                                                                                                                                                                                                                                                                                     *authors Argentin, S.; Nemer, M.; Drouin, J.; Scott, G.K.; Kennedy, B.P.; Davies, P.L. *journal J. Biol. Chem. (1985) 260:4568-4571 *title The gene for rat arrial natriuretic factor. *cross-references MUID:85182558
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Seidman, C.E.; Duby, A.D.; Choi, E.; Graham, R.M.; Haber, Homcy, C.; Smith, J.A.; Seidman, J.G.
Science (1984) 225:324-326
The structure of rat preproatrial natriuretic factor as defined by a complementary DNA clone.
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                                                                                                          #formal_name Rattus norvegicus #common_name Norway rat
19-Feb-1994 #sequence_revision 15-Nov-1984 #text_change
26-Feb-1999
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##residues 1-152 ##label SEI
##cross-references GB:K02062; GB:K02063; NID:g202899; PID:g202900
SNCE A93330
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##residues 1-152 ##label MAK
##cross-references GB:X00665; EMBL:X00658; NID:955711; PID:955712
                                                     natriuretic peptide; atriopeptin I; atriopeptin II; auriculin A; auriculin B; preprocardionatrin
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Nature (1984) 309:719-722
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Tibbetts, C.; Inagam1, T.
                                                                                                                                                                                                                 A22570; A01425; A93332; A43617; A93330; A94275; I
A20973; A44190; A60390; I59094; I58057; I52678
factor precursor - rat
); ANF(3-33); ANF(8-33);
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##residues 1-152 ##label ARG
##cross-references GB:KO2062; NID:9202899; PID:9202900
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##moolecule_type mRNA
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##residues 126-149 ##label ATL
ENCE A94275
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#cross-references MUID:84219798
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Thibault, G.; Murthy, K.K.; Gutkowska, J.; Seidah, N.G.;
Lazure, C.; Chretien, M.; Cantin, M.
Peptides (1988) 9:47-53
NH2-terminal fragment of rat pro-atrial natriuretic factor in
the circulation: identification, radioimmunoassay and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seidah, N.G.; Lazure, C.; Chretien, M.; Thibault, G.; Garcia, R.; Cantin, M.; Genest, J.; Nutt, R.F.; Brady, S.F.; Lyle, T.A.; Paleveda, W.J.; Colton, C.D.; Ciccarone, T.M.; Veber,
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Identification of atrial natriuretic factor gene transcripts
in the central nervous system of the rat.
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K.F.; Adams, S.P.; Eubanks, S.R.; Galluppi, G.R.; Fok, Nedleman, P. Science (1984) 223:67-69
Purification and sequence analysis of bioactive atrial peptides (atriopeptins).
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Sakuragawa, Y.; Nakazato, H.; Fukuda, A.; Minamino, N.;
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#journal Science (1985) 228:323-325
#title Alignment of rat cardionatrin sequences with the preprocardionatrin sequence from complementary DNA.
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Lewicki, J.A.
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#title Amino acid sequence of homologous rat atrial peptides:
natriuretic activity of native and synthetic forms.
#cross-references MID:84194062
#accession A20973
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##residues 25-28,'X',30-31,'X',33,'X',35-38 ##label THI
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##residues 118-150 ##label SE2
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#cross-references MUD:93044510
#accession A60100
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##residues 25-39 ##label BEL
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#accession PT0061
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#product atriopeptin I #status experimental #label ATI\
#product atriopeptin II #status experimental #label AT2\
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*product ANF(3-33) *status experimental *label CN
*product ANF(8-33) *status experimental *label ANF4\
*product auriculin B *status experimental *label AUB\
*product auriculin A *status experimental *label AUB\
*product auriculin A *status experimental *label AUB\
*product atrial natriuretic factor *status predicted
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#title Identification of rat gamma atrial natriuretic polypeptide
and characterization of the cDNA encoding its precursor.
#cross-references MUID:85061500
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#journal Biochem. Biophys. Res. Commun. (1986) 136:396-403
#title Structure and analysis of the bovine atrial natriuretic peptide precursor gene.
#cross.references WID:86215205
#accession A90124
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                                             *authors Ong, H.; McNicoll, N.; Lazure, C.; Seidah, N.; Chretien, M.; Cantin, M.; De Lean A.; Soldan, D. Life Sci. (1986) 38:1309-1315
*title Purification and Sequence determination of bovine atrial matriuretic factor.

*cross-references MUD:86173941
*accession A93049
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*product gamma atrial natriuretic factor #status
predicted #label ANF\
*product alpha atrial natriuretic peptide #status
predicted #label ANP\
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#product gamma atrial natriuretic factor #status
predicted #label ANF\
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experimental *label ANP,
#disulide_bonds *status predicted
*length 152 *molecular-veight 16518 *checksum 7552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #authors Seidman, C.E.; Bloch, K.D.; Klein, K.A.; Smith, J.A.
Seidman, J.G.
#journal Science (1984) 226:1206-1209
#title Nucleotide sequences of the human and mouse atrial natiturelic factor genes.
#cross-references MUID:85065766
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Pred. No. 4.81e+01;
0; Mismatches 0; Indels
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Pred. No. 4.81e+01;
0; Mismatches 0; Indels
##molecule_type DNA
##residues 1-152 ##label VLA
#erross-references GB:M13145; NID:g162665; PID:g162666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##residues 1-152 ##label SEI
##cross-references GB:K02781; NID:9191937; PID:9387099
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##residues 123-150 ##label ONG
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Best Local Similarity 100.0%;
Matches 5; Conservative
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H.; Matsuo, H.
Biochem. Biophys. Res. Commun. (1985) 132:892-899
Structure of dog and rabbit precursors of atrial natriuretic
polypeptides deduced from nucleotide sequence of cloned
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#product gamma atrial natriuretic factor #status
predicted #label ANF\
#product alpha atrial natriuretic peptide #status
predicted #label ANP\
#disulfide_bonds #status predicted
#length 153 #molecular-weight 16843 #checksum 7650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      atrial natriuretic peptide precursor - rabbit
ANP: atrial natriuretic polypeptide
#formal_name Oryctolagus cuniculus #common_name domestic
rabbit
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$14873 *type complete atrial natiluretic peptide precursor - horse strial natiluretic peptide *common_name domestic horse $6.00 *Peb-1995 *sequence_revision 20.Feb-1995 *text_change
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                                                                                                                                                                                                                 Maegert, H.J.; Hanke, M.; Schmeding, G.; Teuteberg, K.; Schulz-Knappe, P.; Forssmann, W.G. submitted to the EMBL Data Library, March 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##molecule_type mRNA
##residues 1-153 ##label OIK
##residues 1-153 ##label OIK
##cross-references GB:M12046; NID:g164770; PID:g164771
CLASSIFICATION #superfamily natriuretic peptide A precursor
KEYWORDS atrium; diuretic; hormone; natriuretic; osmoregulation
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CLASSIFICATION #superfamily natriuretic peptide A precursor
SUMMARX #length 153 #molecular-weight 16825 #checksum
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Pred. No. 4.81e+01;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                        ##status preliminary
##molecule_type mRNA
##residues 1-153 ##label MAE
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#accession B25302
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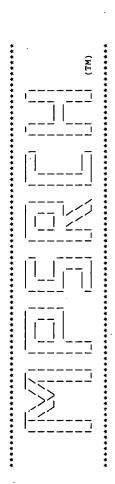
#type complete

I55480

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hypothetical natriuretic peptide/phage fr coat protein mutant fusion protein - synthetic #formal_name synthetic Carnal_name synthetic carnal_name synthetic carnal_name is many and phage fr genes engineered and expressed in Escherichia coli 02-Jul-1996 #sequence_revision 05-Sep-1996 #text_change 155480
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J. Biotechnol. (1993) 30:231-243
High level expression of alpha-human atrial natriuretic factor as a fusion polypeptide with phage fr coat protein in Escherichia coli.
                                                                                                                                                                                               Berzins, V.; Jansone, I.; Skangals, A.; Kalnins, P.; Liepa,
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Brandon, R.C.; Sykes, S.M.; Kaul, S.; Mason, T.M.;
Kerlavage, A.R.; Adams, M.D.; Somerville, C.R.; Venter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T00602 #type complete
hypothetical protein T8K22.8 - Arabidopsis thaliana
#formal_name Arabidopsis thaliana #common_name mouse-ear
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T8K22.8
#length 635 #molecular-weight 72049 #checksum 1480
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Arabidopsis thaliana chromosome II BAC T8K22 genomic
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##cross-references GB:S66567; NID:g435742; PID:g435743
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tbS fusion protein
ty #length 161 #molecular-weight 17287 #checksum 337
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##cross-references EMBL:AC004136; NID:g3184270; PID:g3184278
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed Jun 16 13:23:46 1999; MasPar time 2.01 Seconds 70.179 Million cell updates/Bec Run on:

>US-09-027-777B-3 (1-5) from US09027777B.pep Tabular output not generated.

1 NSFRY 5 Description: Perfect Score: Sequence: 77977 segs, 28268293 residues Searched:

PAM 150 Gap 15

Scoring table:

Minimum Match 0% Listing first 45 summaries Post-processing:

swiss-prot37 1:swissprot Database:

Mean 21.108; Variance 20.967; scale 1.007 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	1.76e+01	1.76e+01	1.76e+01	1.76e+01	1.76e+01	1.76e+01	1.76e+01	1.76e+01	1.76e+01	1.76e+01	1.76e+01	1.76e+01	1.76e+01	1.76e+01	5.00e+01								
Description	ATRIAL NATRIURETIC FAC	60S RIBOSOMAL PROTEIN	60S RIBOSOMAL PROTEIN	60S RIBOSOMAL PROTEIN	ATRIAL NATRIURETIC FAC	FORMATE ACETYLTRANSFER	KETO-ACID FORMATE ACET	TRANSPOSABLE ELEMENT A	HYPOTHETICAL 27.2 KD P	SIGMA-E FACTOR REGULAT	PROLYL-TRNA SYNTHETASE	PROLYL-TRNA SYNTHETASE	PROLYL-TRNA SYNTHETASE	RIBONUCLEOSIDE-DIPHOSP	MYELOPEROXIDASE PRECUR	CATALASE R (EC 1.11.1.							
ID	ANF_CAVPO	RL28_HUMAN	RL28_MOUSE	RL28_RAT	ANF_CANFA	ANF_PIG	ANF_MOUSE	ANF_BOVIN	ANF_RAT	ANF_RABIT	ANF_HUMAN	ANF_HORSE	PFL_CLOPA	TDCE_ECOLI	YAC1_MAIZE	YSHA_ECOLI	RSEB_HAEIN	SYP_METJA	SYP_METTH	SYP_ARCFU	RIR1_BACSU	PERM_MOUSE	CATR_ASPNG
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Result No.	1	7	E	♥	S	ø	7	æ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

Query Match 100.0%; Score 41; DB 1; Length 128; Best Local Similarity 100.0%; Pred. No. 1.76e+01;

5.000+01	5.00e+01	5.00e+01	8.28e+01	8.28e+01	8.28e+01	8.28e+01	8.28e+01	8.28e+01	8.28e+01	8.28e+01	8.28e+01	8.28e+01	8.28e+01	8.28e+01	8.28e+01	8.28e+01	1.35e+02	1.35e+02	1.35e+02	1.35e+02	1.35e+02
MYELOPEROXIDASE PRECHE	KINESIN-LIKE PROTEIN F	CARBAMOYL-PHOSPHATE SY	HEXON-ASSOCIATED PROTE	APOPTOSIS INHIBITOR 1	PUTATIVE PYRROLINE-5-C	RIBONUCLEOSIDE-DIPHOSP	HYPOTHETICAL 47.6 KD P	TRANSCRIPTIONAL REGULA	TRANSCRIPTIONAL REGULA	PUTIDAREDOXIN REDUCTAS	HYPOTHETICAL 49.3 KD P	D(5)-LIKE DOPAMINE REC	INTERFERON-INDUCED 56	GLYCOPROTEIN H PRECURS	TETANUS TOXIN PRECURSO	COLLAGEN ALPHA 1(XII)	ZINC FINGER PROTEIN 37	ZINC FINGER PROTEIN 18	HYPOTHETICAL 85.5 KD P	HYPOTHETICAL 98.3 KD P	HYPOTHETICAL 134.9 KD
DERM HIMAN	FL10_CHLRE	CARB_BACCL	HEX8_ADE12	IAP1_NPVOP	PROC_CAEEL	RIR2_LEIAM	Y47K_BPCHP	NADR_SALTY	NADR_ECOLI	CAMA_PSEPU	Y114_NPVAC	DSDR_FUGRU	INI6_HUMAN	VGLH_HSVMD	TETX_CLOTE	CA1C_CHICK	ZF37_MOUSE	Z184_HUMAN	YBV2_YEAST	YE86_SCHPO	YOO5 CAEEL
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745	786	1065	233	275	299	345	399	409	410	422	424	463	478	813	1314	3124	553	726	753	886	1232
95.1	95.1	95.1	92.7	92.7	92.7	92.7	92.7	92.7	92.7	92.7	93.7	92.7	92.7	92.7	92.7	92.7	90.5	90.2	90.2	90.3	90.2
39	36	39	38	38	38	38	38	38	38	38	38	38	38	38	38	38	37	37	37	37	37
24	52	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

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136 AA; 15602 MW;
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Best Local Similarity 100.0%;
Matches 5; Conservative
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Best Local Similarity 100.0%;
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                                                                                                                                                                                                                                                STANDARD;
                                                               EMBL; X74856; G488835;
                                                                           MGD; MGI:101839; RPL28
                                                                                      RIBOSOMAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIBOSOMAL PROTEIN.
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| NSFRY 5
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SEQUENCE
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RL28_RAT
P17702;
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Gaps
                                                                                                                                                                                                                          TISSUE-COLON;

PRIDLINE; 92290496.

FRIGERIO J.M., DAGORN J.C., IOVANNA J.L.;

"Cloning, sequencing and expression of the L5, L21, L27a, L28, S5, S9, S10 and S29 human ribosomal protein mRNAs.";

BICCHIM. BIOPHYS. ACTA 1265:64-68(1995).

-! SIMILARITY: BELONGS TO THE L28E FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BURKE P.S., LIUM E., LIN C.S., WOLGEMUTH D.J.;
"Sequence and expression of a cDNA encoding the mouse homologue o
"Inbosomal protein L28.";
GENE 142:315-316(1994)
-:- SIMILARITY: BELONGS TO THE L28E FAMILY OF RIBOSOMAL PROTEINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                  HOMO SAPIENS (HUMAN).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41; DB 1; Length 136;
Pred. No. 1.76e+01;
0; Mismatches 0; Indels
Indels
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75D1BB8F CRC32;
                                                                         3 STANDARD; PRT; 136 AA. PR105: 01-FEB-1995 (REL. 31, CREATED) 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE) 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE) 60S RIBOSOMAL PROTEIN L28.
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          136 AA; 15630 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%;
Matches 5; Conservative
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5; Conservative
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MEDLINE; 94252590.
                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                     122 NSFRY 126
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                                   1 NSFRY 5
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ANE_CANEA STANDARD; PRT; 149 AA.

P07499;
01-APR-1988 (REL. 07, CREATED)
01-APR-1998 (REL. 07, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-SPRAGUE-DAWLEY: TISSUE-LIVER;
MEDLINE: 91002678.
WOOL I.G., CHAN Y.-L., PAZ V., OLVERA J.;
"The primary structure of rat ribosomal proteins: the amino acid sequences of L27a and L28 and corrections in the sequences of S4 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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-!- SIMILARITY: BELONGS TO THE L28E FAMILY OF RIBOSOMAL PROTEINS.
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EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA: MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE: RATIUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41; DB 1; Length 136;
Pred. No. 1.76e+01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41; DB 1; L4
Pred. No. 1.76e+01;
0; Mismatches 0;
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ECEC217C CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1990 (REL. 15, CREATED)
01-FFB-1991 (REL. 17, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
60S RIBOSOMAL PROTEIN 128.
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SEQUENCE FROM N.A. MEDLINE; 85065766
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P05125;
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  "The
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01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
01-6CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 85124561.
FORSZBANN W.G., BIRR C., CARLQUIST M., CHRISTMANN M., FINKE R.,
HENSCHEN A., HOCK D., KIRCHHEIM H., KREYE V., LOTTSPEICH F., METZ J.,
MUTT V., REINECKE M.;
                                                                                                                                                                                                             polypeptides deduced from nucleotide sequence of cloned cDNA.";
BIOCHEN. BIOPHYS. RES. COMMUN. 132:892-899(1985).
-!- FUNCTION: ATRIAL NATRIBETIC FACTOR (ANF) IS A POTENT VASOACTIVE
SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAEGERT H.J., APPELHANS H., GASSEN H.G., FORSSMANN W.G.;
"Nucleotide sequence of a porcine prepro atrial natriuretic peptide
(ANP) cDNA.";
                                                                                                                                                                                                                                                                                                                                           A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS. SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
                                                                                                                                                                                                                                                                                                  KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
                                                                                                                                                                  OIKAWA S., IMAI M., INUZUKA C., TAWARAGI Y., NAKAZATO H., MATSUO "Structure of dog and rabbit precursors of atrial natriuretic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                      CANIS FAMILIARIS (DOG).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
CARNIVORA; FISSIPEDIA; CANIDAE; CANIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
ARTIODACTYLA; SUIFORMES; SUINA; SUIDAE; SUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41; DB 1; Length 149;
Pred. No. 1.76e+01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15819 MW; D4F3A6CF CRC32;
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PFAM; PF00212; ANP; 1.
VASOACTIVE; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
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ANP) (PREPRONATRIODILATIN)
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Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M12045; G163901; -.
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                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 86076957.
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NSFRY 5
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DISULFID
SEQUENCE
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ANF_PIG
P24259;
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01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BY SIMILARITY).
ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
BY SIMILARITY.
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-I- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
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               an endocrine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARDIODILATIN-RELATED PEPTIDE (CDP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleotide sequences of the human and mouse atrial natriuretic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 85065766.
SEIDMAN C.E., BLOCH K.D., KLEIN K.A., SMITH J.A., SEIDMAN J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
myocardiocytes of the heart constitute an endo
srization of a porcine cardiac peptide hormone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41; DB 1; Length 150;
Pred. No. 1.76e+01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4FF67B94 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S13107; S13107.
PROSITE; PSG0263; NATRIURETIC_PEPTIDE; 1.
PFAM; PF00212; ANP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-AUG-1987 (REL. 05, CREATED)
13-AUG-1987 (REL. 05, LAST SEQI
01-OCT-1996 (REL. 34, LAST ANNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16351 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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145
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54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VASOACTIVE; SIGNAL. SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-1988 (REL. 07, CREATED)
01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
ATRIAL MATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
(ANP) (PREPRONATRIODILATIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIFE SCI. 38:1309-1315(1986).
-!- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE
SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS TROUGHT TO PLAY A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Purification and sequence determination of bovine atrial natriuretic factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTIVITY.

A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS.

SIMILARITY: BELONGS TO THE NATRIORETIC PEPTIDES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE, 86173941.
ONG H., MCNICOLL N., LAZURE C., SEIDAH N., CHRETIEN M., CANTIN M., DE LEAN A.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BOS TAURUS (BOVINE).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
ARTIODACTYLA; RUMINANTIA; PECORA; BOVOIDEA; BOVIDAE; BOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VLASUK G.P., MILLER J., BENCEN G.H., LEWICKI J.A.; "Structure and analysis of the bovine atrial natriuretic peptide
                                                                                                                                                                                                                                                ö
                                                                                                                AURICULIN A (BY SIMILARITY).
AURICULIN B (BY SIMILARITY).
ATRIOPEPTIN I (BY SIMILARITY).
BY SIMILARITY.
5163CB23 CRC32;
                                                                                                                                                                                                      Score 41; DB 1; Length 132;
Pred. No. 1.768+01;
...arthes 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BIOCHEM. BIOPHYS. RES. COMMUN. 136:396-403(1986).
                                                                                                                                                                                                                                                                                                                                                                 152 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
PFAM; PF00212; ANP; 1.
                         PIR; A29370; AWMS.
MGD; MGI-97367; NPPA.
PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
PFAM; PF00212; ANP; 1.
                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                         MW.:
                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%;
Matches 5; Conservative
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               EMBL; K02781; G387099; -
                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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150
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                                                                                                                              126
127
127
129
159 AA;
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                                                                               VASOACTIVE; SIGNAL.
SIGNAL
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1 NSFRY 5
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P07501;
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DISULFID
SEQUENCE
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21-UL-1986 (REL. 01, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
ATRIAL MATRIURETIC FACTOR PRECURSOR (ANF) (ARRIAL NATRIURETIC PEPTIDE)
(ANP) (PREPRONATRIODILATIN) (CONTAINS: AURICULINS; ATRIOPEPTINS).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDILINE; 84550178.
MEDILINE; 84550178.
SEIDMAN C.E., DOBY A.D., CHOI E., GRAHAM R.M., HABER E., HOMCY C.,
SMITH J.A., SEIDMAN J.G.;
"The structure of rat preproatrial natriuretic factor as defined by
SCIENCE 225:324-326(1984).
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIVIN R.A., CONDRA J.H., DIXON R.A.F., SEIDAH N.G., CHRETIEN M., NEMER M., CHAMBERLAND M., DROUIN J.;
"Molecular cloning and characterization of DNA sequences encoding and human atrial natriuretic factors.",
PROC. NATL. ACAD. SCI. U.S.A. 81:6325-6329(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Structure of rat atrial natriuretic factor precursor deduced from
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A..
MEDILIB: 84219797.
YAMANAKA M., GREENBERG B., JOHNSON L., SEILHAMER J.J., BREWER M.,
FRIEDEMANN T., MILLEF J., ATLAS S.A., LARAGH J., LEWICKI J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KANGAWA K., TAWARAGI Y., OIKAWA S., MIZUNO A., SAKURAGAWA Y., NAKAZAO H., FUKUDA A., NINAMINO N., MATSOO H. "Identification of rat gamma atrial natiuretic polypeptide and characterization of the CDNA encoding its precursor.";
                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                          FIDDES J.C.; "Cloning and sequence analysis of the cDNA for the rat atrial natriuretic factor precursor."; NATURE 309:719-722(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŠEÓUENCE FROM N.A.
MEDLINE; 84219798.
MAKI M., TAKAYANAGI E., MISONO K.S., PANDEY K.N., TIBBETTS C.
INAGANI T.;
                                                                                                                                                                                                                                                                                                                                   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE; 85182558.
ARGENTIN S., NEMER M., DROUIN J., SCOTT G.K., KENNEDY B.P.,
DAVIES P.L.;
                                       Score 41; DB 1; Length 152;
Pred. No. 1.76e+01;
0; Mismatches 0; Indels
145
16518 MW; CF200882 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The gene for rat atrial natriuretic factor.
                                                                                                                                                                                               152 AA
                                                                                                                                                                                               PRT;
                                           Query Match
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA sequence.";
NATURE 309:722-724(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NATURE 312:152-155(1984).
                                                                         5; Conservative
                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                     RATIUS NORVEGICUS (RAI).
129 1
152 AA;
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                                                                                                     146 NSFRY 150
                                                                                                                                 1 NSFRY 5
DISULFID
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ANF_RAT
PO1161;
                                                                         Matches
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PEPTIDE
PEPTIDE
PEPTIDE
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AC PO
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                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 84194062.
SEIDAH N.G., LAZURE C., CHRETIEN M., THIBAULT G., GARCIA R.,
CANTIN M., GENEST J., NUTT R.F., BRADY S.F., LYLE T.A., PALEVEDA W.J.,
COLTON C.D., CICCARONE T.M., VEBER D.F.; TALIA peptides: natriuretic
activity of native and synthetic forms...
PROC. NATL. ACAD. SCI. U.S.A. 81:2640-2644(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
                                                                                                                                                                                                                    ATIAS S.A., KLEINERT H.D., CAMARGO M.J., JANUSZEWICZ A., SEALEY J.E., LARAGH J.H., SCHILLING J.W., LEWICKI J.A., JOHNSON L.K., MAACK T.; "Purification, sequencing and synthesis of natriuretic and vasoactive
                                       elucidation of the structure of atrial natriuretic factor, a new
                                                                                                           MEDLINE; 87175636.
GARDNER D.G., VLASUK G.P., BAXTER J.D., FIDDES J.C., LEWICKI J.A.;
"Identification of atrial natriuretic factor gene transcripts in the central nervous system of the rat.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "NH2-terminal fragment of rat pro-atrial natriuretic factor in the circulation: identification, radioimmunoassay and half-life."; PEPTIDES 9:47-53(1988).
                                                                                                                                                                                                                                                                                                                    MEDLINE; 84097513.
CURRIE M.G., GELLER D.M., COLE B.R., SIEGEL N.R., FOK K.F.,
ADAMS S.P., EUBANKS S.R., GALLUPPI G.R., NEEDLEMAN P.;
"Purification and sequence analysis of bioactive atrial peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 88203350.
THIBAULT G., MURTHY K.K., GUTKOWSKA J., SEIDAH N.G., LAZURE C.,
CHRETIEN M., CANTIN M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
                                                                                                                                                               PROC. NATL. ACAD. SCI. U.S.A. 84:2175-2179(1987).
                                                                                                                                                                                         AURICULINS, SEQUENCE, AND SYNTHESIS OF 126-149. MEDLINE: 84219796.
                                                                    CAN. J. PHYSIOL. PHARMACOL. 65:2013-2020(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
PFAM; PF00212; ANP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AURICULIN A.
                                                                                                                                                                                                                                                                                                       SEQUENCE OF 127-149, AND SYNTHESIS.
                                                                                              SEQUENCE OF 38-152 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M15868; G202904; -.
                                                                                                                                                                                                                                                            rat atrial peptide.";
NATURE 309:717-719(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X00665; G55712; -. EMBL; X02062; G202900; - EMBL; X01118; G55717; -. EMBL; M27498; G202906; -
                                                                                                                                                                                                                                                                                                                                                                                        SCIENCE 223:67-69(1984).
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149
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 118-150.
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PIR; A44190; A44190.
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SIGNAL 1
PEPTIDE 126
  SEQUENCE FROM N.A. MEDLINE; 88109092.
              88109092.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 25-38
                                                       peptide hormone.
                                                                                                                                                                                                                                                                                                                                                                              (atriopeptins).
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                            FLYNN T.G.;
                                          The
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between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE: 86076957.
OIKAWA S., IMAI M., INUZUKA C., TAWARAGI Y., NAKAZATO H., MATSUO H.;
OIKAWA S., IMAI M., INUZUKA C., TAWARAGI Y., NAKAZATO H., MATSUO H.;
Sfructure of dog and rabbit precureors of atrial natriuretic
polypeptides deduced from nucleotide sequence of cloned cDNA.";
BIOCHEM. BIOPHYS. RES. COMMUN. 132:892-899(1985).
-1- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE
SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
ACTIVITY.
ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP)
                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORYCTOLAGUS CUNICULUS (RABBIT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
LAGOMORPHA; LEPORIDAE; ORYCTOLAGUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 41; DB 1; Length 153;
Pred. No. 1.76e+01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                              Length 152;
                                                                                                                                                                                       0; Indels
                                                                                                                                              Score 41; DB 1; L
Pred. No. 1.76e+01;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153 AA; 16843 MW; 1FA4FB42 CRC32;
AURICULIN B.
ATRIOPEPTIN I.
ATRIOPEPTIN II.
ATRIOPEPTIN III.
                                                                                                      2D424B75 CRC32;
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                                                                                                                                                                                                                                                                                                                                                              153 AA.
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ANE-HUMAN STANDARD;
A01-10160;
21-JUL-1986 (REL. 01, CREATED)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ANP) (PREPRONATRIODILATIN).
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                                                                                                                                            100.0%;
similarity 100.0%;
5; Conservative
                                                                                                         16556
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126
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152 AA;
                                                                                                                                              Ouery Match
Best Local Similarity
Matches 5; Conser
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1 NSFRY 5
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PROSITE; PS0
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P07500;
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PDB; 1ANP;
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P27104;
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DISULFID
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SEQUENCE
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    용
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13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
(ANP) (PREPRONATRIODILATIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rat
                                                                                                                                                                                                      MEDLINE; 84219799.
OIKAWA S., IMAI M., UENO A., TANAKA S., NOGUCHI T., NAKAZATO H., KANGAWA K., FUKUDA A., MATSUO H.;
"Cloning and sequence analysis of cDNA encoding a precursor for human atrial natriuretic polypeptide.";
NATURE 309:724-726(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KANGAWA K., MATSUO H.;
"Purification and complete amino acid sequence of alpha-human atrial natriuretic polypeptide (alpha-hANP)";
BIOCHEM. BIOPHYE. RES. COMMUN. 118:131-139(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Nucleotide sequence of the gene encoding human atrial natriuretic
factor precursor.";
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                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 84295577.
NARAYAMA K., OHKUBO H., HIROSE T., INAYAWA S., NAKANISHI S.; "RRNA sequence for human cardiodilatin-atrial natriuretic factor precursor and regulation of precursor mRNA in rat atria."; NATURE 310:699-701(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-151 FROM N.A. MEDELINE 85065766. SEIDMAN J.G., SEIDMAN J.G., SEIDMAN G.E., BLOCH K.D., KLEIN K.A., SMITH J.A., SEIDMAN J.G., "Nucleotide sequences of the human and mouse atrial natriuretic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRUCTURE BY NMR OF 124-151 MUTANT SELECTIVE FOR NPR-C RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning of genomic DNA for human atrial natriuretic factor.";
BIOCHEM. BIOPHYS. RES. COMMUN. 125:797-802(1984),
                                                                                                       HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S., DROUIN J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE: 85061627.
GREENBERG B.D., BENCEN G.H., SEILHAMER J.J., LEWICKI J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ERRINGTON H.;
SUBMITTED (MAY-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEMER M., CHAMBERLAND M., SIROIS D., ARGENTIN S., D
DIXON R.A.F., ZIVIN R.A., CONDRA J.H.;
"Gene structure of human cardiac hormone precursor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and human atrial natriuretic factors."; PROC. NATL. ACAD. SCI. U.S.A. 81:6325-6329(1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85096983.
PARMENTIER M., INAGAMI T.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            factor genes.";
SCIENCE 226:1206-1209(1984).
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-151 FROM N.A. MEDLINE; 84295577.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                factor precursor.";
NATURE 312:656-658(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pronatriodilatin.";
NATURE 312:654-656(1984).
                                                                                                     (HUMAN)
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                                                                                        VPPA OR PND
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01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
                                                                                                                                                                                                                                                       -: THE HUMAN GENOME CONTAINS 2 DIFFERENT PREPRONATRIODILATIN GENES ONE CODES FOR 2 ARG RESIDUES AT THE C-TERMINUS THAT ARE CLEAVED TO FORM THE MATURE PEPTIDE, WHILE THE OTHER ENDS IN A TERMINATION CODON IMMEDIATELY AFTER THE LAST CODON OF THE MATURE EPTIDE.
-: SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
BY SIMILARITY.
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MAEGERT H.J., RICHTER R., SCHMAEDING G., FORSSMANN W.G.;
SUBMITTED (MAR-1991) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE
                                                                                                                -!- FUNCTION: ATRIAL NATIONELIC FACTOR (ANF) IS A POTENT VASOACTIVE SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY REY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
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FAIRBROTHER W.J., MCDOWELL R.S., CUNNINGHAM B.C.; "Solution conformation of an atrial natriuretic peptide variant selective for the type A receptor."; BIOCHEMISTRY 33:8897-8904(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISSING (IN ONE OF THE TWO GENES)
C24A68AF CRC32;
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PERISSODACTYLA; EQUIDAE; EQUUS.
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Pred. No. 1.76e+01;
0; Mismatches 0;
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VASOACTIVE; SIGNAL: 3D-STRUCTURE: 1 25
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K02044; G178632; -.
AL021155; E1294859; -.
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Best Local Similarity 100.0%;
Matches 5; Conservative
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146.
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152
153 AA;
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Query Match
Best Local Similarity 100.0%;
Matches 5; Conservative
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01-NOV-1988 (REL.
15-DEC-1998 (REL.
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P42632;
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P08771;
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                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
ATRIAL NATIURETIC PEPTIDE, ALPHA (ANP).
BY SINILARITY
FESDSF4A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                   A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS. SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
FORMATE ACETYLTRANSFERASE (EC 2.3.1.54) (PIRUVATE FORMATE-LYASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLOSTRIDIUM PASTEURIANUM.
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; CLOSTRIDIACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- PATHWAY: GLUCOSE METABOLISM (NONOXIDATIVE CONVERSION).
-!- SUBUNIT: HOMODIMER (BY SIMILARITY)
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-!- SIMILARITY: STRONG, TO OTHER PYRUVATE FORMATE-LYASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    + PYRUVATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WEIDNER G., SAWERS G.; "Molecular characterization of the genes encoding pyruvate formate-lyase and its activating enzyme of Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41; DB 1; Length 153;
Pred. No. 1.76e+01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BACTERIOL. 178:2440-2444(1996).
- CATALYTIC ACTIVITY: ACETYL-COA + FORMATE - COA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      740 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; S14873; S14873.
PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16825 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X58563; G1009; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00212; ANP; 1. VASOACTIVE; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 1
130 . 1
153 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WEDLINE; 96218720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pasteurianum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147 NSFRY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLOSTRIDIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LT 13
PFL_CLOPA
Q46266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEPTIDE
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
KETO-ACID FORMATE ACETYLTRANSFERASE (EC 2.3.1.-) (KETO-ACID FORMATE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1988 (REL. 09, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
TRANSPOSABLE ELEMENT ACTIVATOR HYPOTHETICAL 12 KD PROTEIN (AC 12 KD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STATIN-KIZ / MG1655;
MEDLINE; 97426617.
BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,
RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESCHERICHIA COLI.
BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
ESCHERICHIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HESSLINGER C., FAIRHURST S.A., SAWERS G.;
UNPUBLISHED OBSERVATIONS (XXX-1997).
-!- PATHWAY: ANAEROBIC PATHWAY THAT DEGRADES L-THREONINE TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE000393; Ost. EMBL; ECCGENE; EG12758; TDCE.
PROSITE: PS00850; GLY_RADICAL; 1.
PFAM: PF01228; GLY_RADICAL; 1.
FRANSPERASE; ACYLTRANSFERASE; ORGANIC RADICAL.
TRANSPERASE; ACYLTRANSFERASE; ORGANIC (BY SIMILARITY).

RAT31 MW; DA3FA991 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSMAD B., SHAO Y.;
"The complete genome sequence of Escherichia coli K-12.";
SCIENCE 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 41; DB 1; Length 746; Best Local Similarity 100.0%; Pred. No. 1.76e+01; Matches 5; Conservative 0; Mismatches 0; Indels
Length 740;
                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-!- SIMILARITY: STRONG, TO PYRUVATE FORMATE-LYASES.
   Score 41; DB 1; Lv
Pred. No. 1.76e+01;
                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                      746 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09, CREATED)
09, LAST SEQU
37, LAST ANNO
                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U18997; G606055; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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Search completed: Wed Jun 16 13:23:53 1999 Job time: 7 secs.

71 NTFRY 75

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protein - protein database search, using Smith-Waterman algorithm Wed Jun 16 13:24:09 1999; MasPar time 4.08 Seconds 66.914 Million cell updates/sec MPsrch_pp Run on:

>US-09-027-777B-3 (1-5) from US09027777B.pep 41 1 NSFRY 5 Title: Description: Perfect Score: Sequence:

Tabular output not generated.

PAM 150 Gap 15 Scoring table:

Minimum Match 0% Listing first 45 summaries Post-processing:

179066 segs, 54579741 residues

Searched:

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus sptremb19 Database:

scale 0.873 Mean 20.285; Variance 23.245; Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ			•		
Result No.	Score	Query	Query Match Length DB	DB	ID	Description	Pred. No.
ਜ 	41	100.0	110	-	058195	110AA LONG HYPOTHETICA	5.47e+01
7	41	100.0	151	4	013766	ATRIAL NATRIURETIC FAC	5.47e+01
m	41	100.0	152	9	046540	ATRIAL NATRIURETIC PEP	5.47e+01
4	41	100.0	155	9	029130	CARDIODILATIN, ATRIAL	5.47e+01
S	41	100.0	164	œ	P92530	ORF164.	5.47e+01
9	41	100.0	195	S	044830	F54D12.6 PROTEIN.	5.47e+01
7	41	100.0	513	ď	032561	KETO ACID FORMATE-LYAS	5.47e+01
80	41	100.0	635	10	064715	T8K22.8 PROTEIN.	5.47e+01
σ	41	100.0	. 993	S	P91157	COSMID C44C3.	5.47e+01
10	39	95.1	79	7	056386	HYPOTHETICAL 9.2 KD PR	1.41e+02
11	39	95.1	107	-	058090	107AA LONG HYPOTHETICA	1.41e+02
12	6€	95.1	141	10	P93305	ORF141.	1.41e+02
13	39	95.1	190	'n	077421	FEMALE-SPECIFIC HISTAM	1.41e+02
14	60	95.1	209	14	012300	REPLICASE.	1.41e+02
15	6€	95.1	240	7	031875	YOSN PROTEIN.	1.41e+02
16	60	95.1	254	13	091307	MYOSIN VI (FRAGMENT).	1.41e+02
17	6 6	95.1	256	2	061766	C35E7.8 PROTEIN.	1.41e+02
18	ტ ტ	95.1	293	14	096615	BV1 AND BC1 GENES, COM	1.41e+02
19	39	95.1	297	13	091296	MYOSIN VI (FRAGMENT).	1.41e+02
50	39	95.1	310	7	066675	ADP-L-GLYCERO-D-MANNO-	1.41e+02

1.41e+02	1.41e+02	1.41e+02	1.41e+02	1.41e+02	1.41e+02	1.41e+02	1.41e+02	1.41e+02	1.41e+02	1.41e+02	1.41e+02	1.41e+02	1.41e+02	1.41e+02	1.41e+02	1.41e+02	1.41e+02	1.41e+02	1.41e+02	1.41e+02	1.41e+02	1.41e+02	1.41e+02	1.41e+02
T24A6.4 PROTEIN.	CYSTEINE PROTEINASE.	CYSTEINE PROTEINASE.	CYSTEINE PROTEINASE.	CYSTEINE PROTEINASE 1	F36H12.2 PROTEIN.	GTP-BINDING PROTEIN.	M.BSSHII METHYLASE.	HYPOTHETICAL 48.7 KD P	NOSD PROTEIN.	HNF-3/FORK-HEAD TRANSC	F58G1.7 PROTEIN.	589AA LONG HYPOTHETICA	WEE1-LIKE KINASE.	F59F5.3 PROTEIN.	UNIDENTIFIED FERRIC SI	REPLICASE.	PUTATIVE DIPEPTIDYL AM	DELTA-ENDOTOXIN.	FERRICHROME-IRON RECEP	CARBOMYLPHOSPHATE SYNT	HYPOTHETICAL 120.7 KD	INDUCIBLE NITRIC OXIDE	PUTATIVE MINOR TAIL PR	ORF40.
061946	046031	046032	046030	095029	076720	P96085	030877	005912	031383	013606	062270	058168	046149	021046	P94274	012301	014073	045755	P72599	050302	013807	054705	080179	034071
Ŋ	2	2	S	ß	S		7	~	7	m	'n	-	ស	S	~	14	m	7	7	7	m	11	6	~
315	331	331	338	341	350	360	375	439	453	517	569	589	614	671	724	729	793	803	863	1064	1072	1149	1510	1517
95.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1	35.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1	95.1
39	39	39	39	39	39	39	39	39	39	39	39	36	39	39	39	39	39	39	36	39	39	39	39	39
21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	4	45

ALIGNMENTS

RESULT TO O O O O O O O O O O O O O O O O O

Gaps

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EUKARYOTA, VIRIDIPLANTAE, STREPTOPHYTA, EMBRYOPHYTA, TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA, MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAÈNORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE: CAENORHABDITIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41; DB 8; Length 164;
Pred. No. 5.47e+01;
                                                                                                                                                                              Length 155;
                                                                                                                                                                                Score 41; DB 6; Length 155; Pred. No. 5.47e+01; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                 PARDIGOL A.;
SUBMITTED (MAR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL.; 270294; E233859; -.
PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
PFAM; PF00212; ANP; 1.
SEQUENCE 155 AA: 16860 MW; 77E8CA8B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06, CREATED)
06, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1997 (TREMBLREL. 03, CREATED)
01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
01-MAY-1997 (TREMBLREL. 03, LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
UNSELD M., MARIENFELD J.R., BRANDT P., BRENNICKE in NAT. GENET. 0:0-0(0).
EMBL, Y08502; EZ83579; -.
MITOCHONDRION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             164 AA; 18341 MW; E294F940 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195 AA
                                                                                                                                                                                                                                                                                                                                                                                                                    164 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARABIDOPSIS THALIANA (MOUSE-EAR CRESS) MITOCHONDRION.
                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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Best Local Similarity 100.0%;
Matches 5; Conservative
                                                                                                                                                                              Query Match
Best Local Similarity 100.0%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1998 (TREMBLREL.
01-JUN-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
F54D12.6 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BRISTOL N2;
MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149 NSFRY 153
                                                                                                                                                                                                                                                                             149 NSFRY 153
  TISSUE-HEART;
                                                                                                                                                                                                                                                                                                           1 NSFRY 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 NSFRY 5
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P92530
P92530;
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                                                                                                                                                                                                                                                                                                                         CARDIODILATIN-RELATED PEPTIDE (CDP).
ATRIAL NATRIURTIC PEPTIDE, ALPHA (ANP).
BY SIMILARITY.
BY 8827DA3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OVIS ARIES (SHEEP).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
ARTIODACTYLA; RUMINANTIA; PECORA; BOVOIDEA; BOVIDAE; CAPRINAE; OVIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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AITKEN G.D., RAIZIS A.M., GEORGE P.M., ESPINER E.A., CAMERON V.A.;
SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF037465; G2708650; -.
PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
SEQUENCE 152 AA; 16368 MW; D5360BCC CRC32;
                                       SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEDIANO C.E., BLOCH K.D., ZISFEIN J., SMIT J., HABER E., HOMCY C.,
SEIDMAN C.E., BLOCH E., GRAHAM R.M., SEIDMAN J.G.;
"MOJECULAR STUDIES Of the atrial natriuretic factor gene.";
"MOJECULAR STUDIES OF THE ATRIAL NATRIURETIC FACTOR GENE.";
EMBL: M54947, G178638;
EMBL: M54947, G178638;
EMBL: M54951; G178638;
FENDI: PFONTELS STORES TO THE TO TH
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
CARDIODILATINA TRIAL NATRIURETIC PEPTIDE.
TUPATA BELANGERI.
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
SCANDENTIA; TUPAIIDAE; TUPAIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41; DB 6; Length 152;
Pred. No. 5.47e+01;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41; DB 4; Length 151;
Pred. No. 5.47e+01;
0; Mismatches 0; Indels
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SCHNEIDEMANN S., MAEGERT H.J., FORSSMANN W.G.;
SUBMITTED (MAR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                            151 AA; 16381 MW;
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046540;
01-JUN-1998 (TREMBLREL. 06, C
01-JUN-1998 (TREMBLREL. 06, L
01-AUG-1998 (TREMBLREL. 07, L
ATRIAL NATRIURETIC PEPTIDE.
CATARRHINI; HOMINIDAE; HOMO.
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Best Local Similarity 100.0%;
Matches 5; Conservative
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Best Local Similarity 100.0%;
Matches 5; Conservative
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1 NSFRY 5
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PEPTIDE
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WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., EAVELLO A., FULTON L.,
CRAXTONER A., GREEN P., HAWINTS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAM J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTWING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., FOOFBA A., SOUNDERS D., SHOWKEEN R.,
SMALDON N., SMITH A., SONNHAAMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
ROUNSLEY S.D., LIN X., KETCHUM K.A., CROSBY M.L., BRANDON R.C
SYKES S.M., KAUL S., MASON T.M., KERLAVAGE A.R., ADAMS M.D.,
SOMERVILLE C.R., VENTER J.C.;
SOMENTIED (JUN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, ACO04136; 63184278; -
SEQUENCE 635 AA; 72049 MW; 07FC643C CRC32;
                                                                                                                                                        Score 41; DB 10; Length 635 Pred. No. 5.47e+01; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41; DB 5; Length 993;
Pred. No. 5.47e+01;
0; Mismatches 0; Indels
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EMBL; U80028; G1699137; -.
SEQUENCE 993 AA; 115001 MW; A6FCFA5E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
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01-NOV-1996 (TREMBLREL. 01,
01-NOV-1996 (TREMBLREL. 01,
01-NOV-1998 (TREMBLREL. 08,
HYPOTHETICAL 9.2 KD PROTEIN.
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Best Local Similarity 100.0%;
Matches 5; Conservative
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Best Local Similarity 100.0%;
Matches 5; Conservative
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01-MAY-1997 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
WATERSTON R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-BRISTOL N2;
MEDLINE; 94150718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
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Q56386
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P91157
P91157;
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EUKARYOTA; VIRIDIRLANNAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
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ESCHERICHIA.
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Pred. No. 5.47e+01;
                                                                                                                                                                                                                                                                                                       Score 41; DB 5; Length 195;
Pred. No. 5.47e+01;
0; Mismatches 0; Indels
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                                                                                                                                                                                                         WATERSTON R.;
SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, TF040647; G2746630; -
SEQUENCE 195 AA: 22009 MW; 8COB0769 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN~W3110;
HESSLINGER C., SAWERS G.;
SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HESSLINGER C., FAIRHURST S.A., SAWERS G.;
SUBMITTED (SEP-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AJ001620; E1169787; -
                                                                                              MAGGI L., GOELA D.;
SUBMITTED (JAN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
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07, LAST ANNOTATION UPDATE)
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SEQUENCE 513 AA; 58248 MW; A8023A3E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            513 AA.
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Local Similarity 100.0%;
hes 5; Conservative
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      NATURE 368:32-38(1994).
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STRAIN=CV. COLUMBIA;
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                                                SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T8K22.8 PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                             .138 NSFRY 142
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01-JUL-1997 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 AA;
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NSFRY 5
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1 NSFRY 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PYROCOCCUS HORIKOSHII.
ARCHAEA: EURYARCHAEOTA; THERMOCOCCALES; THERMOCOCCACEAE; PYROCOCCUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete Sequence and Gene Organization of the Genome of a Hyper-thermophilic Archaebacterium, Pyrococcus horikoshii OT3."; DNA RES. 5:55-76(1998). EMBL: AP0000012; D1030369; -. SEQUENCE 107 AA; 11348 MW; D4781A0C CRC32;
                                                                                                                                     RASMUSSEN J.L., ODELSON D.A., MACRINA F.L.;
"Complete nucleotide sequence of insertion element IS4351 from Bacteroides fragilis."
J. BACTERIOL, 169:3573:3580(1987).
EMBL: M17124; G1197008: -.
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                                   SEQUENCE FROM N.A.
TRANSPOSON-TRANSPOSON TN4351;
RASMUSSEN J.L.
SUBMITTED (JUL-1988) TO EMBL/GENBANK/DDBJ DATA BANKS.
BACTEROIDES FRAGILIS.
BACTERIA; CYTOPHAGALES; BACTEROIDACEAE; BACTEROIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P93305,
P93305,
01-MAY-1997 (TREMBLREL. 03, CREATED)
01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
01-JAN-1999 (TREMBLREL. 09, LAST SHOUTATION UPDATE)
ORFI41.
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11-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
107AA LONG HYPOTHETICAL PROTEIN.
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Pred. No. 1.41e+02;
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SEQUENCE 79 AA; 9166 MW; 9E31B22F CRC32;
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TRANSPOSON-TRANSPOSON TN4351;
MEDLINE; 87279905.
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larity 80.0%;
Conservative
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Similarity 80.0%;
4; Conservative
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Best Local Similarity
Matches 4; Conserv
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MEDLINE; 98344137.
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VIRUSES; SSRNA POSITIVE-STRAND VIRUSES, NO DNA STAGE; TOMBUSVIRIDAE;
CARMOVIRUS.
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MEDILIES, 98166875.
CIUFFREDA P., RUBINO L., RUSSO M.;
"Molecular cloning and complete nucleotide sequence of galinsoga mosaic virus genomic RNN.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUKARYOTA; METAZOA; ARTHROPODA; CHELICERATA; ARACHNIDA; ACARI;
PARASITIFORMES; IXODIDA; IXODIDAE; RHIPICEPHALUS.
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TISSUE-SALIVARY GLAND;
PAESEN G.C., NUTTALL P.A.;
"A family of histanine-binding salivary proteins from the tick, Rhiptoephalus appendiculatus.";
SUBMITTED (APR-1997) TO EMBL/GENBANK/DDBJ DAIA BANKS.
EMBL; U96001; G3452089;
                                                                                                                                                                                   Length 141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 39; DB 5; Length 190; Pred. No. 1.41e+02; 1; Mismatches 0; Indels
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Best Local Similarity 80.0%; Pred. No. 1.41e+02;
Matches 4; Conservative 1; Mismatches 0; Indels
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[1]
SEQUENCE FROM N.A.
UNSELD M., MARIENFELD J.R., BRANDT P., BRENNICKE A.;
UNAT. GENET.
EMBL; Y08501; E283595; -.
MENDEL; 13049; ARAth; 2249; 1.
SEQUENCE 141 AA; 16689 MW; 956EBE94 CRC32;
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SUBMITTED (MAY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
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Pred. No. 1.41e+02;
1; Mismatches 0;
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SEQUENCE 209 AA; 22949 WW; 4D31DD75 CRC32;
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01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UP
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION
FEMALE-SPECIFIC HISTAMINE-BINDING PROTEIN 2.
RHIPICEPHALUS APPENDICULATUS.
                                                                                                                                                                                                                                                                                                                                                                                                                    190 AA.
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Best Local Similarity 80.0%;
Matches 4; Conservative
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Best Local Similarity 80.0%;
Matches 4; Conservative
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AZEVEDO V., BERTERO M.G., BESSIERES P., BOLDTIN A., BORCHERT S., AZEVEDO V., BERTERO M.G., BESSIERES P., BOLDTIN A., BORCHERT S., BONSTIER L., BANNS A., BRANN M., BRIGNEL S.C., BRON S., BORNEISER L., BANNS A., BRANN M., BRIGNEL S.C., BRON S., BORNIES R. L., BOUNETRO V., CAPUNO V., CARTER N.M., CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A., DENIZOT F., DEVINER K.M., DUSTERHOFT A., EMRILCH S.D., EMMERSON P.T., ENTIAN K.D., ERRINGTON J., FABRET C., FERRAIL E., FOULGER D., GALLERON N., GUISEPPI G., GUY B.J., HAGAR K., HAIRERT H., HOLSAPPEL S., HOSONO S., HARNOD C.R., HENDUT A., JORIS B., KARAMATA D., KASAHARA Y., KIAERR-BLANCHARD M., KLEIN C., ANDEATSHIY Y., KOETTER P., KONINGSTEIN G., KROGH S., KUABRO M., ALLEYINE A., LAPIDUS A., LANDININS S., LAUBER J., LAZARENIC V., LAPIDUS A., LANDININS S., MAUEL C., MEDIGUE C., PUNIC P. PUNRELLE B., RAPOPORT G., REY M., SADAIE Y., SCANLAN E., SCHLEUR B., ROSE M., SADAIE Y., SCHLEUR A., TAKCOLI A., TAKCONI E., TAKAGI T., TAKAMARA T., TAKAMARU K., SCHLEUR B., ROSE M., SADAIE Y., SCHLEUR B., TAKAGI T., TAKAMARA T., TAKAMARA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BACILLUS SUBTILIS.
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match

95.1%; Score 39; DB 2; Length 240;
Best Local Similarity 80.0%; Pred. No. 1.41e+02;
Matches 4; Conservative 1; Mismatches 0; Indels
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SUBNITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; 299114; E1185478; .
PFAM: PF00317; ribonucleo_red; 1.
SEQUENCE 240 AA; 27966 MW: 16160EDD CRC32;
                                                                                                                                                                                                                                                                                                                                                01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
YOSN PROTEIN.
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                                                                                                                                                                                                                                                                     PRELIMINARY;
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MEDLINE; 98044033
29 NAFRY 33
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| NSFRY 5
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Search completed: Wed Jun 16 13:24:43 1999 Job time : 34 secs.

231 NAFRY 235

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Rat pre-proANVP. Sequence of pre-pro-a

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2.95e-18
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6.70e-16
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P51102 P51107 P51107 P51107 P51128 P60017 P50128 P50128 P50112 P60159 P60159 P61103 P61103

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**************************************	Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd	
MPsrch_pp protein - pr	protein - protein database search, using Smith-Waterman algorithm	
Run on: Wed Jun	Wed Jun 16 12:47:54 1999; MasPar time 4.58 Seconds	
Tabular output not generated	•	
Title: >VANDER Description: (1-37) Perfect Score: 279 Sequence: 1 LRALI	>VANDER-027-213.PEP (1-37) from vander027777.pep 279 1 LRALLTAPRSLRRSSFRCGRWDRIGAQSGLGGNSFRY 37	
Scoring table: PAM 150 Gap 11	-	<u> </u>
Searched: 170751	segs, 21266608 residues	
Post-processing: Minimum Match 0% Listing first 45 summaries	Match 0% first 45 summaries	
Database: a-geneseq35 1:part1 2 8:part8 9 14:part19 19:part19 24:part29 34:part39 34:part39	eneseq35 :part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 :part8 9:part19 10:part10 11:part11 12:part113 :part8 15:part15 part16 17:part17 18:part18 4:part14 15:part20 21:part21 22:part22 23:part23 4:part24 25:part25 26:part26 27:part27 28:part28 9:part29 30:part30 31:part31 32:part32 33:part33 4:part34 35:part35 36:part36 37:part37 38:part38	

secretion
Claim 22; Page 16; 35pp; German.
This variant of the peptide described in P50491 has a mol.wt.
This variant of the peptide described in P50491 has a mol.wt.
of 13,000 and an isoelectric point of 6.6.5. This peptide
hormone, as well as its C-terminal fragments obtained by
partial bromcyan separation between the Met groups and
behind the latter, has strong relaxation activity on smooth
vasomuscles. It also affects sweat secretion and can be used for
the diagnosis and therapy of hypertension. It can also be used for
the treatment of post-operative cardiovascular disorders, skin
diseases, etc. The hormone may be prepared from a heart atrium
struct. See also P50491-2. Gaps WPI: 85-171361/28. New peptide hormone cardiodilatine - from atrium tissue having effects on heart muscle ionotropy, smooth muscle, and sweat ö Score 279; DB 3; Length 88; Pred. No. 2.60e-21; 0; Mismatches 0; Indels P50493; 18-MAR-1992 (first entry) Cardiodilatine peptide hormone variant. Cardiodilatine; peptide; hormone; hypotensive; WO8502850-A. 88 37 52 lralltaprslrrsscfggrmdrigaqsglgcnsfry T 1 P50493 standard; protein; 88 AA. Query Match 100.0%; Best Local Similarity 100.0%; Matches 37; Conservative 21-DEC-1984; D00279. 24-DEC-1983; DE-346953. (ORGA-) ORGANGEN MED MOL. Forssmann WG; RESULT g NAME OF THE PROPERTY OF THE PR à

1 LRALLTAPRSLRRSCFGGRMDRIGAOSGLGCNSFRY

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Cardiodilatine peptid
Human atrial natriure
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Sequence of human gam
Human pre-proANVP #2.
Sequence of pre-human
Human pre-proANVP #1.
Sequence of the precu
Cardiodilatin peptide
Sequence encoded by h

P50493 W34533 P501240 P501340 R00582 R36935 R36936 P50030 P50050 P70629 P50050 P70629 P50050

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279 279 279 279 279 279 279 267 267 267 267 267 267

Sequence of pre-pro-a Sequence of pre-pro-a Rat atrial natriureti recombinant pro-c

P50115 P60165

Pred. No.

Description

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Length

Query Match

Score

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Mean 24.237; Variance 85.878; scale 0.282

Statistics:

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JT 2 W34533 standard; Protein; 126 RESULT ü

Gaps

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Vesely

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The inventors claim a polypeptide comprising atrial natriuretic/vasodilator polypeptide (ANVP), pro-ANVP or pre-pro-ANVP, or their fragments. The encoding DNA sequence is also claimed. The claimed polypeptides are natriuretics, diuretics, vasodilators and modulators of the renin-angiotensin-aldosterone system. Dose is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The precursor of human gamma-ANP and its 26Asn-151Tyr fragmentare calaimed (P50036, p50037), as are the DNA SOS encoding them (N50020, N50055). The 26Asn-151Tyr fragment has a diuretic action so is useful as a hypotensive/antihypertensive agent. The usual dose is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Monoclonal antibodies recognising gamma-atrial natriuretic used for diagnosis of diseases eg kidney and heart disease. Disclosure, Fig.1: 10pp; English. Gamma-halv of which the N-terminal 25 AAs are recognisy monoclonal antibodies of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-SEP-1991 (first entry)
Sequence of human gamma-atrium natriuretic polypeptide (ANP).
Natriuretic; diuretc; hypotensive; antihypertensive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; N50055.
New DNA sequences from human atrium cordis - coding for new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 126;
                                                                                                                                                                                                                                                            Length 126
                                                                                                                                                                                                                                                     Score 279; DB 4; Length 126
Pred. No. 2.60e-21;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human gamma atrial natriuretic polypeptide (gamma-hANP)
Gamma atrial natriuretic polypeptide; ANP; natriuretic;
hypertension; cirrhosis; nephrosis; heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-JUN-1984; 116605.
08-JUN-1984; DT-116605.
08-JUN-1984; DT-116605.
(SUNR ) SUNTORY LTD.
Matsuc H, Kangawa K, Hayashi Y, Oikawa S, Oshima 'Y
Tanaka S, Nakazato H, Tawaragi Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 279; DB 3; Le
Pred. No. 2.60e-21;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90 lralltaprslrrsscfggrmdrigagsglgcnsfry 126
                                                                                                                                                                                                                                                                                                                                                                                     90 lralltaprslrrsscfggrmdrigaqsglgcnsfry 126
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                                                                                                                                                                                                                                                                                                                                                                                                                      1 LRALLTAPRSLRRSSCFGGRMDRIGAQSGLGCNSFRY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diuretic polypeptide or precursor cpds. Claim 26; Page 37; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-JAN-1988.
30-JUN-1989; 306669.
04-JUL-1988; JP-166641.
(SHIO) Shlonogi Selyaku Kabushiki.
Imura H, Nakao K;
WPI; 90-009970/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .r 5
R00582 standard; protein; 126 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T 4
P50037 standard; Protein; 126 AA.
                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 100.0%;
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 37; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 AA;
                                                                                                                                                         0.01-100 ug/kg.
Sequence 126 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
EP-350227-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-1 mg/kg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      refugent of hypertension and related disorders - with synthetic peptide fragment of atrial natriuretic factor pro:hormone Disoure; Column 4: 19pp; English.

Disclosure; Column 4: 19pp; English.

Confidence represents the human atrial natriuretic factor prohormone (proANF). Fragments of this sequence (see W34521-W34523) can be used in the method of the invention. The method is for treating hypertension, congestive heart failure, pulmonary oedema, toxeamia of pregnancy.

Consisting of amino acids 1-30, 31-67 or 79-98 of proANF. The peptides constitution of amino acids 1-30, 31-67 or 79-98 of proANF. The peptides by prekalaemia associated with acidosis, digitalis overdose, succinylcholine, insulin deficiency, acute or chronic renal failure, durents, natriuretic and/or kalluretic activity.

Sequence 126 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                              Human atrial natriuretic factor prohormone.
Human atrial natriuretic factor prohormone; therapy; hypertension; congestive heart fallure; pulmonary oedema; toxaemia of pregnancy; nephrotic syndrome; renal fallure; hepatic cirrhosis; hyperkalaemia; acidosis; digitalis overdose; insulin deficiency; Addison's disease; proANF; hyperaldosteronism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 2.60e-21;
0; Mismatches 0; Indels
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Sequence of pro-atrial natriuretic/vasodilator polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1984; US-616488.
20-JUN-1984; US-616488.
20-JUN-1984; US-622639.
61-JUN-1984; US-622639.
61-JUN-1984; US-622639.
61-JUN-1984; US-628654/46.
61-JUN-1985-289654/46.
61-JUN-1985-289654/46.
61-JUN-1985-289658, vasodilators and modulators of the renin-angiotensin-aldosterone system claim 8; Page 116; 144pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Natruiretic; duiretic; vasodilator;
venin-angiotensin-aldosterone-system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P51240 standard; peptide; 126 AA.
P51240;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%;
Matches 37; Conservative
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                                (first entry)
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                                                                                                                                                                                                                                                                                                                                          09-MAR-1995; 401246.
09-MAR-1995; US-401246.
29-SEP-1987; US-102477.
01-MAY-1990; US-517252.
14-NOV-1991; US-799211.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-NOV-1985.
16-APR-1985; U00658.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (VESE/) VESELY D L.
Vesely DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 98-017684/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disulfide_bond
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                                                                                                                                                                                                                                                     Homo saptens
US5691310-A.
W34533;
24-Mar-1998
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Gaps

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Indels

Mammal.

(ANNP)

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Sequence

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New DNA sequences from human atrium cordis - coding for new diuretic polypeptide or precursor cpds.

Claim 25; Fig 5; S19p; Bnglish.

The precursor of human gamma-ANP and its 26Asn-151Tyr fragmentare claimed (P50036, P50037), as are the DNA SQs encoding them (N50020,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 1A; 45pp; English.

This sequence is encoded by the human pre-pro atrial natriuretic/vasodilator peptide (ANVP) DNA. Fragments of this protein and the corresponding sequence in rat (see also R36936), may be used for regulation of fluid volume and blood pressure in host organisms.

The ANVP fragments may be produced by solid-phase techniques. See
                                                                                                                                                                              Human, pre-pro; atrial natriuretic/vasodilator peptide; ANVP; rat; regulation; fluid volume; blood pressure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptide cpd. - useful as natriuretic, dluretic and/or vasodilator in mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-SEP-1991 (first entry)
Sequence of the precursor of human gamma-atrium natriuretic polypeptide (ANP).
Natriuretic; diuretc; hypotensive; antihypertensive.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 279; DB 7; Length 151;
Pred. No. 2.60e-21;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matsuo H, Kangawa K, Hayashi Y, Oikawa S, Oshima
Tanaka S, Nakazato H, Tawaragi Y;
             147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 lralltaprslrrsscfggrmdrigaqsglgcnsfry 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LRALLTAPRSLRRSSCFGGRMDRIGAQSGLGCNSFRY 37
            /note= "Signal peptide"
                                                                                                                                                                                                                                                                                  42..151
/note= "Mature protein"
                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                    08-MAY-1985; US-766030.
05-JUN-1986; US-870795.
(SCIO) SCIOS NOVA INC.
Lewicki JA. SCarborough RM;
WPI; 93-175525/21.
N-PSDB; Q44454.
                                                                                                 T . 8
R36934 standard; Protein; 151
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Best Local Similarity 100.0%;
Matches 37; Conservative
                                                                                                                                                 14-SEP-1993 (first entry)
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08-JUN-1984; 116605.
08-JUN-1984; JP-116606.
08-JUN-1984; JP-116605.
(SUNR ) SUNTORY LTD.
                                                                                                                                                                                                                                                                                                                                                                      US-602117.
US-616488.
                                                                                                                                                                    Human pre-proANVP #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            also R36937-78
                                                                                                                                                                                                                                                                                                                                   18-MAY-1993.
09-APR-1984; 6
09-APR-1984; U
                                                                                                                                                                                                                 Homo sapiens.
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Physio-active peptide derived from birds - has cysteine bridge, specified As sequence and diuretic and antihypertensive properties. Disclosure; Fig 14; 16pp; Japanese.
This sequence has 99 amino acid residues homologous to the pre-chANP. See also 003466-003468, R03301 and R03402.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polypeptide cpd. - useful as natriuretic, diuretic and/or vasodilator in mammals
Disclosure; Fig 1B; 45pp; English.
This sequence is encoded by the human pre-pro atrial natriuretic/vasodilator peptide (ANVP) cDNA. Fragments of this protein and the corresponding sequence in rat (see also R3695), may be used for regulation of fluid volume and blood pressure in host organisms. The ANVP fragments may be produced by solid-phase techniques. See
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                                                                  Gaps
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US5212286-A.
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                               ; DB 2; Length 126; 2.60e-21;
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                                                                Indels
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Pred. No. 2.60e-21;
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                                 Score 279;
                                                  Pred. No.
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R36935 standard; Protein; 136
R36935;
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Best Local Similarity 100.0%;
Matches 37; Conservative
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Best Local Similarity 100.0%;
Matches 37; Conservative
                             Query Match
Best Local Similarity 100.0%;
Matches 37; Conservative
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14-JUL-1988; 173739.
14-JUL-1988; JP-173739.
                                                                                                                                                                                                                                                                                                                                                      09-APR-1984; 602117.
09-APR-1984; US-602117.
01-JUN-1984; US-616488.
08-MAY-1985; US-766030.
                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUN-1986; US-870795
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                                                                                                                                                                                                                                                    Human pre-proANVP #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 AA;
126 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            also R36937-78
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Seguence

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02025499-A.

R03301;

18-MAY-1993.

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Gaps

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P51239;
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Disclosure: Fig. 13; 45pp; English.
The DNA encoding the cardiodilatin is carried on plasmid pHANR48.
Cardiodilatin is a muscle relaxant, so is useful as an antihypertensive agent: The DNA is obtd. from RNA isolated from the human heart.
Sequence 151 AA;
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                                13
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Cardiodilatin peptide.
Cardiodilatin; plasmid pHANF48; muscle relaxant; antihypertensive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human atrial natriuretic peptide factor (ANF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genetic analysis diagnostic for hypertension - by detecting polymorphous of the renin, kallikrein or ANF gene regions bisclosure; Fig 2; 51pp; Egglish; Ergish are the patent application is for a method used for determn. Of a genetic fingerprint of a subject which allows early diagnosis of
N50055). The 26Asn-151Tyr fragment has a diuretic action so is useful as a hypotensive/antihypertensive agent. The usual dose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Expression vector contg. gene for cardionatrin or cardiodilatin corresp. DNA sequences, useful as antihypertensive agents.
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12-CCT-1984; JP-213897.
(MITU) Mitebubishi Chemical Industries Ltd.
Nakanishi S, Teranishi Y, Nagahari K, Shibui T, Takamatsu K;
WPI; 85-271495/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 279; DB 3; Length 151;
Pred. No. 2.60e-21;
0; Mismatches 0; Indels
                                                                                                                                                             Length 151;
                                                                                                                                                                                                                     Indels
                                                                                                                                                Score 279; DB 3; Le
Pred. No. 2.60e-21;
0; Mismatches 0;
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P70629 standard; protein; 151 AA
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11-JUN-1986; US-873199.
(BIOT-) BIOTECHN RES PARTN.
Shine J. Baker AR, Frossard PM;
WPI; 87-136035/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                       T 10
P50050 standard; protein; 151
P50050;
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Best Local Similarity 100.0%;
Matches 37; Conservative
                                                                                                                                                      Ouery Match 100.0%;
Best Local Similarity 100.0%;
Matches 37; Conservative
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24-OCT-1986; U02293.
24-OCT-1985; US-790813.
12-NOV-1985; US-796904.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-APR-1985; 400726.
12-APR-1984; JP-073663.
21-JUN-1984; JP-128335.
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                                                                                        151 AA;
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WO8702709-A.
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                                                                 01-1 mg/kg.
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This sequence was isolated from a cDNA library prepared from poly(A) mRNA isolated from human heart. Sequences complementary to the DNA encoding MERIG of cardionatrin were isolated using maxture of oligonucleotide probes. Two plasmids, phAYD and phMANP, identified by this screening process, were then used to transform E.coli which were cultured to produce the peptide.
                                                                                                                                                                                                                                                Gaps
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individuals at risk of hypertension and permits early therapeutic measures to prevent the fatal symptomology of the disease. The section of the genome which is fingerprinted or otherwise subject is study using the results is dependent on the nature of the probe. The probes useful in the present invention are selected from the renin, kallikrein, or ANF gene (see FT).
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Sequence of pre-pro-atrial natriuretic/vasodilator polypeptide
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                                                                                                                                                                       Score 275; DB 2; Length low Pred. No. 7.39e-21;
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116-APR-1985; U00658.
19-APR-1984; US-602117.
01-JUN-1984; US-616488.
20-JUN-1984; US-622639.
(BIOT) BIOTENHOL RESPENT.
Johnson LK, Atlas SA, Mccarthy BJ, Laragh JH, Lewicki JA;
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Best Local Similarity 100.0%; Pred. No. 5.96e-20;
Matches 36; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                             115 lralltaprslrrsscfggrmdrigaesglgcnsfry 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Natruiretic; duiretic; vasodilator;
venin anglotensin-aldosterone-system.
Mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-NOV-1990 (first entry)
Vascodilatory peptide, cardionatrin.
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P51239 standard; peptide; 150 AA.
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18-SEP-1986, 220835.
18-SEP-1986, JP-220835.
(MITU) MItsubishi Chem Ind KK.
WPI; 88-170991/25.
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                                                                                                                                                                                           Query Match
Best Local Similarity 97.3%;
Matches 36; Conservative
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P82656 standard; protein;
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J63107997-A.
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Query Match
Best Local Similarity 91.9%;
Matches 34; Conservative
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                 New atrial poly:peptide cpds. - useful as natriuretics, diuretics, vasodilators and modulators of the renin-angiotensin-addosterone system (Claim 7: Page 115: 144pp; English.

The inventors claim a polypeptide comprising atrial natriuretic/vasodilator polypeptide (ANVP), pro-ANVP or pre-pro-ANVP, or their pragments. The encoding DNA sequence is also claimed. The claimed polypeptides are natriuretics, diuretics, vasodilators and modulators of the renin-angiotensin-aldosterone system. Dose is
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New atrial poly:peptide cpds. - useful as natriuretics, diuretics, vasodilators and modulators of the renin-angiotensin-aldosterone system

Example: Fig 1A: 144pp: English.

The inventors claim a polypeptide comprising atrial natriuretic/ vasodilator polypeptide (ANVP), pro-ANVP or pre-pro-ANVP, or their fragments. The encoding DNA sequence is also claimed. The claimed polypeptides are natriuretics, diuretics, vasodilators and modulators of the renin-anglotensin-aldosterone system. Dose is
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Pred. No. 5.96e-20;
0; Mismatches 0; Indels
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01-JUN-1984; US-616488.
01-JUN-1984; US-622639.
(BIOT-) BIOTECHNOL RES PART.
JOHNSON LK, ALIAS SA, MCCARTHY BJ, Laragh JH, Lewicki JA; WPI; 85-289654/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-AUG-1992 (first entry)
Sequence of pre-pro-atrial natriuretic/vasodilator
Polypeptide (ANVP).
Natruiretic; duiretic; vasodilator;
venin-angiotensin-aldosterone-system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-001-1991 (first entry)
Rat atrial natriuretic factor-beta.
Atrial natriuretic factor; diuretic; hypotensive.
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misc_difference 16..41
/note= "encoded by N50763"
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P51241 standard; peptide; 150 AA
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P50115;
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Best Local Similarity 100.0%;
Matches 36; Conservative
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Sequence 150 AA;
85-289654/46
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atrium cordis.
Claim 1; Page 17; 23pp; English.
The rat atrial natriuretic factor-beta has diuretic, natriuretic and hypotensive or hypertensive activity.
Sequence 43 AA;
                                                                      28-FEB-1985; 301364.
02-MAR-1984; JP-038816.
65UNR) SUNTORY LTD.
MALSUO H, Kabawa K;
WPI; 85-218548/36.
New diuretic, antihypertensive polypeptide - isolated from rat
                                                                                                                                                                                                                                                                                                                                                                                 Score 264; DB 3; Length 48;
Pred. No. 1.30e-19;
3; Mismatches 0; Indels
disulfide_bond 27..43
                             EP-153865-A.
04-SEP-1985.
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Gaps

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Search completed: Wed Jun 16 12:48:39 1999 Job time: 45 secs.

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F. Collins, Biocomputing Researd 9-1998 University of Edinburgh, ion rights by Oxford Molecular Li in database search, using Smith-v	Run on: Wed Jun 16 12:51:39 1999; MasPar time 1.79 Seconds Tabular output not generated.	Title: >VANDER-027-213.PEP Description: (1-37) from vander027777.pep Perfect Score: 279 Sequence: 1 LRALLTAPRSLERSSCFGGRMDRIGAQSGLGCNSFRY 37	Scoring table: PAM 150 Gap 11	Searched: 106580 segs, 10152877 residues	Post-processing: Minimum Match 0% Listing first 45 summaries	Database: a-issued 1:5A_COWB 2:5B_COMB 3:PCT9_COMB 4:backfiles1	Statistics: Mean 22.667; Variance 80.942; scale 0.280	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES Result Query No. Score Match Length DB ID Description Pred. No.	279 100.0 136 4 5212286-4 279 100.0 151 4 5212286-5 252 90.3 144 4 520239-1 252 90.3 144 4 520239-1 242 86.7 32 4 5449751-3 242 86.7 32 4 5449751-1 242 86.7 32 1 0S-08-451-1 242 86.7 32 1 0S-08-451-1 242 86.7 32 2 0S-08-737-1 251 79.2 32 1 0S-08-451-1 251 79.2 32 1 0S-08-470-1 251 79.2 32 1 0S-08-470-1 251 77.4 28 1 0S-08-451-1 256 77.4 28 1 0S-08-297-1 256 77.4 28 1 0S-07-754-1 256 77.4 28 1 0S-07-754-1 257 77.4 28 1 0S-07-828-1 257 77.4 28 1 0S-07-828-1

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9.53e-14
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                  Patent No. 5461142.
Sequence 2, Applicatio
Sequence 21, Applicatio
Sequence 21, Applicatio
Sequence 21, Applicatio
Sequence 1, Applicatio
Sequence 1, Applicatio
Sequence 9, Applicatio
Sequence 9, Applicatio
Sequence 3, Applicatio
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Pred. No. 8.03e-22;
0; Mismatches 0; Indels
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APPLICANT: LEMICKI, JOHN A.; SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
PEPTIDE COMPUNDS

NUMBER OF SEQUENCES: 68
CURRENT 'APPLICATION DATA:
APPLICATION NUMBER: US/07/870,795
FILING DATE: 05-JUN-1986
PRIOR APPLICATION DAMER: 766,330
FILING DATE: 08-MAY-1985
APPLICATION NUMBER: 602,117
FILING DATE: 09-APR-1984
APPLICATION NUMBER: 616,488
CONTROL OF FILING DATE: 01-JUN-1984
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LENGTH: 136
SEQUENCE 147 AA; 15978 MW; 112999 CŅ;
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                                                                          US-07-754-
US-08-451-
PCT-US94-0
US-08-448-
5204327-3
US-08-470-
US-07-754-
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US-07-754-

US-08-240-

US-08-240-

PCT-US94-1

US-07-781-

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US-07-781-

US-07-781-

US-07-781-

US-07-781-

US-08-451-

PCT-US94-1
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Best Local Similarity 100.0%;
Matches 37; Conservative
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XX XXXXXX
AC XXXXXX
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XX AX APPLICY
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                                           TITLE OF INVENTION: EXPRESSION OF RECOMBINANT POLYPEPTIDES IMPROVED PURIFICATION
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7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: FORSSMANN, WOLF-GEORG; ALT, JEANETTE M.; BECKER, GENHARD; HERBEST, FRANZ
TITLE OF INVENTION: CARDIODILATIN FRAGMENT, PROCESS FOR NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,240
FILING DATE: 24-3N-1994
PRIOR APPLICATION ADATA:
APPLICATION NUMBER: 994,084
APPLICANT: TARNOWSKI, JOSEPH S.;HILLIKER, SANDRA; WILLETT, SCOTT W.
                                                                                                                                                                                                                          5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 252; DB 4; Length 144; Pred. No. 9.03e-19;
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Pred. No. 9.03e-19;
1; Mismatches 0; Indels
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                                                      WITH IMPROVED PURIFICATION
NUMBER OF SEQUENCES: 16
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/564,259
FILING DATE: 07-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WITH IMPROVED PURIFICATION
NUMBER OF SEQUENCES: 16
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/564,259
FILLING DATE: 07-AUG-1990
SEQ ID NO:3:
LENGTH: 144
                                                                                                                                                 LENGTH: 144
VCE 156 AA; 17116 MW; 129679 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 AA; 17:115 MW; 129665 CN;
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Best Local Similarity 92.3%;
Matches 36; Conservative
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Best Local Similarity 92.3%;
Matches 36; Conservative
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5202239-3
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5449751-3
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ID 54
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Pred. No. 4.01e-20;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                      Length 151;
                                                                                                                                                                                                                                                                                                     Indels
 APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M. TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR PEPTIDE COMPUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 5212286
APPLICANT: LEWICKI, JOHN A.; SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: ATRIAL NATRIURETIC/VASODILATOR
PEPTIDE COMPUNDS
NUMBER OF SEQUENCES: 68
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Pred. No. 8.03e-22;
0; Mismatches 0.
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                                        CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/870,795
FILING DATE: 05-UNH-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 766,030
FILING DATE: 09-APR-1984
APPLICATION NUMBER: 602,117
FILING DATE: 09-APR-1984
APPLICATION NUMBER: 616,488
FILING DATE: 01-JUN-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/07/870,795
FILING DATE: 05-JUN-1986
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 766,030
FILING DATE: 08-MAY-1985
APPLICATION NUMBER: 602,117
FILING DATE: 09-APR-1984
APPLICATION NUMBER: 616,488
FILING DATE: 01-JUN-1984
                                                                                                                                                                                                                                                                                                                                                                                                                            165 AA
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                                                                                                                                                                                                                         LENGTH: 151
ICE 164 AA; 17827 MW; 143008 CN;
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Best Local Similarity 91.9%;
Matches 34; Conservative
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Best Local Similarity 100.0%;
Matches 37; Conservative
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                                                                                                                                                                                                              SEQ ID NO:2
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ID 5202239-1
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Sequence 4, Application US/08737927

Patent No. 5767239

GENERAL INFORMATION:
APPLICANT: IMMER, Hansueli
APPLICANT: ADERMANN, Wolf-Georg
APPLICANT: ALESSEN, Christian
TITLE OF INVENTION: PROCESS AND INTERNEDIATE PRODUCTS FOR
TITLE OF INVENTION: PREPARING CARDIODILATIN FRAGMENTS, AND HIGHLY PURIF.
TITLE OF INVENTION: CARDIODILATIN FRAGMENTS, AND HIGHLY PURIF.
NUMBER OF SEQUENCES: 5
                      APPLICANT: Oare, pavid
APPLICANT: McDowell, Robert S.
APPLICANT: McDowell, Robert S.
APPLICANT: Burnier, John
TITLE OF INVENTION: PECEPTOR SPECIFIC ATRIAL NATRIURETIC
TITLE OF INVENTION: PEPTIDES
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 32;
                                                                                                                                                                                                                                                                                                                                                                      COUNTRI.
21P: 94080-
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
MEDIUM TYPE: 5.25 compatible
~~worther: IBM PC compatible
~~ DC-DOS/NS-DOS
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Pred. No. 1.20e-17;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/451,240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TAPRSLRRSSCFGGRMDRIGAQSGLGCNSFRY 32
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                                                                                                                                                                                                                                                                   STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/362552
FILING DATE: 06-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/152994
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOGY: linear
32 AA; 3508 MW; 4652 CN;
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Cunningham, Brian
                                                                                                                                                                                                                                            Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 415/225-8228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
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Best Local Similarity 100.0%;
Matches 32; Conservative
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                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: FORSSMANN, WOLF-GEORG;ALT, JEANETTE M.;BECKER, GERHARD;HERBEST, FRANZ TITLE OF INVENTION: CARDIODILATIN FRAGMENT, PROCESS FOR PREPARING SAME AND USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 242; DB 4; Length 32;
Pred. No. 1.20e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                      Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                   Score 242; DB 4;
Pred. No. 1.20e-17;
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                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,240
FILING DATE: 24-JAN-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TAPRSLRRSSCFGGRMDRIGAQSGLGCNSFRY 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08451240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 AA; 3838 MW; 6483 CN;
                         APPLICATION NUMBER: 795,248
FILING DATE: 18-NOV-1991
APPLICATION NUMBER: 401,401
FILING DATE: 01-SEP-1989
APPLICATION NUMBER: 100,144
FILING DATE: 28-AUG-1987
                                                                                                                                                                                                                                            LENGIH: 32
4CE 35 AA; 3838 MW; 6483 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 994,084
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: 795,248
FILING DATE: 18-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 401,401
FILING DATE: 01-SEP-1989
APPLICATION NUMBER: 100,144
FILING DATE: 28-AUG-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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Best Local Similarity 100.0%;
Matches 32; Conservative
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                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%;
Matches 32; Conservative
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                                                                                                                                                                                                                   SEQ ID NO:3
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SEQUENCE

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APPLICANT: Lowe, David G.
APPLICANT: Countingham, Brian C.
APPLICANT: Oare, David G.
APPLICANT: Burnier, David G.
APPLICANT: Burnier, John
TITLE OF INVENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC PEPTIDES
NUMBER OF SEQUENCES: 43
ANDERESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                       Score 242; DB 3; Length 32;
Pred. No. 1.20e-17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 AA
                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Genearceh, Inc.
STREET: 460 Polint San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
21P: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,846A
FILING DATE: 06-Jun-1995
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SSOFTWARE: PALIN (Genentech)
SSOFTWARE: PALICATION NATA:
APPLICATION NUMBER: PCI/US94/12591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TAPRSLRRSSCFGGRMDRIGAQSGLGCNSFRY 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WinPatin (Genentech)
                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/152994
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JMBER: 08/419877
11 APR-1995
                                                                                                                                                                                                                                                                                                                                          32 AA; 3508 MW; 4652 CN;
                                                                                                                                                                               32,637
                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 8
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                   TELEPHONE: 415/225-1249
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                : 32 amino acids
amino acid
                                                                                                                                                               NAME: Winter, Daryl B. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
FILING DATE: 11-APR-1
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Best Local Similarity 100.0%;
Matches 32; Conservative
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MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Genent
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                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LT 11
US-08-470-846A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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APPLICANT: Cowe, David
APPLICANT: Lowe, David
APPLICANT: Cunningham, Brian C.
APPLICANT: Gener, David
APPLICANT: McDowell, Robert S.
APPLICANT: Burnier, John
TITLE OF INVENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 242; DB 2; Length 32;
Pred. No. 1.20e-17;
0; Mismatches 0; Indels
                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/737,927
               SEE: Nikaido, Marmelstein, Murray & Oram
: 655 Fifteenth Street N.W. Suite 330
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Genentech, Inc.
STRET: 460 Point San Bruno Blvd
STRET: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                     CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 95/33769
FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application PC/TUS9412591
GENERAL INFORMATION:
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JENCE 32 AA; 3508 MW; 4652 CN;
                                                                                                                                                                                                                                                                                                              36,105
                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION TELEPHONE: (202)638-5000
                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                       (202)638-4810
                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                        STATE: D.C.
COUNTRY: U.S.A.
2IP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                NAME: Kitts, Monica C
REGISTRATION NUMBER:
   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 86.7%;
Best Local Similarity 100.0%;
Matches 32; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                          FILING DATE:
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ID PCT-US94-12591-2
                ADDRESSEE:
STREET: 65
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Gaps

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Sequence 5, Application PC/TUS9412591
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Lowe, David
APPLICANT: Cunniqham, Brian C.
APPLICANT: Cunniqham, Brian C.
APPLICANT: McDowell, Robert S.
APPLICANT: Burnier, Javid
APPLICANT: Burnier, SPECIFIC ATRIAL NATRIURETIC
TITLE OF INVENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC
TITLE OF INVENTION: PEPTIDES
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
                                                                                                                                                                                                                                                                                                                                                                                                    Length 32;
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                 Score 221; DB 2; 1
Pred. No. 2.67e-15;
1; Mismatches 1
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/12591
                                                                                                                      P0844P2C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 TAPRSLRRSSCFGGRMDRIGAQSGLGCNSFRY 37
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APPLICATION NUMBER: 08/152994
PILING DATE: 12-NOV-193
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Daryl B.
REGIGTRATION NUMBER: 32,637
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application PC/TUS9412591
                                                                                         REGISTRATION NUMBER: 36,575
REGISTRATION NUMBER: 96,575
REEEPHONE: 415,225-8228
TELEPHONE: 415,925-9881
TELEFAX: 910,731-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                TOPOLOGY: Linear
CE 32 AA; 3589 MW; 4484 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FELECOMMUNICATION INFORMATION TELEPHONE: 415/225-1249
    APPLICATION NUMBER: 08/15
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                               Kubinec, Jeffrey
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 79.2%;
Best Local Similarity 93.8%;
Matches 30; Conservative
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DE Sequence 5, Applice
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CC GENERAL INFORMATI
CC APPLICANT: CON
CC CONMUTER FEADAL
CC CONMUTER EADAL
CC COMPUTER: IN
CC COM
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                                                                               NAME:
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Patent No. 5846932
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Cunningham, Brian C.
APPLICANT: Cunare, David G.
APPLICANT: Obser, David G.
APPLICANT: Obser, David G.
APPLICANT: Obser, David G.
APPLICANT: Burnier, John
TITLE OF INVENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC PEPTIDES
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTY: LOSA
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 86.7%; Score 242; DB 2; I
Best Local Similarity 100.0%; Pred. No. 1.20e-17;
Matches 32; Conservative 0; Mismatches 0;
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/362552
FILING DATE: 06-JAN-1995
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/152994
FILING DATE: 12-NOV-1993
ATTORNEY JAENT INFORMATION:

NAME: Kubinec, Jeffrey S.

RECISTANION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: 90844P2C1
TELEPHONE: 415/225-8228
TELEPHONE: 415/225-8228
TELEPHONE: 415/225-828
TELEFROMEY: 910/371-7168
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/470,846A FILING DATE: 06-Jun-1995 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TAPRSLRRSSCFGGRMDRIGAQSGLGCNSFRY 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 TAPRSLRRSSCFGGRMDRIGAQSGLGCNSFRY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/362552 FILING DATE: 06-JAN-1995
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APPLICATION NUMBER: 08/419877
FILING DATE: 11-APR-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: Linear
ICE 32 AA; 3508 MW; 4652 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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LENGTH: 32 amino acids
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US-08-470-846A-5
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Search completed: Wed Jun 16 12:51:46 1999 Job time : 7 secs.
Query Match
Best Local Similarity 93.8%;
Matches 30; Conservative
                                                                                                                                                                                                                Patent No. 5449751.
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5449751-2
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APPLICANT: Cundingham, Brian
APPLICANT: Cundingham,
APPLICANT: McDowell, Robert S.
APPLICANT: Burnier, John
APPLICANT: APPLICANTION: PEPTIDES
TITLE OF INVENTION: PEPTIDES
CORPRESSORMER: 47
                                                                                           Length 32;
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                           Score 221; DB 3;
Pred. No. 2.67e-15;
1; Mismatches 1
                                                                                                                                                                                                                              32 AA.
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,240
                                                                                                                                                 1 TAPRSLRRSSCFGGRIDRIRAQSGLGCNSFRY 32
                                                                                                                                                              6 TAPRSLERSSCFGGRMDRIGAGSGLGCNSFRY 37
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: 460 Point San Buno Blvd
South San Francisco
California
                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/08451240 Patent No. 5665704 GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION UNBER: 08/362552
FILING DATE: 06-JAN-1995
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/08451240
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32 AA; 3589 MW; 4484 CN;
                                                        JOGY: linear
32 AA; 3589 MW; 4484 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
                          LENGTH: 32 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Kubinec, Jeffrey REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER
 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                           Query Match
Best Local Similarity 93.8%;
Matches 30; Conservative
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TITLE OF INVENTION: CARDIODILATIN FRAGMENT, PROCESS FOR PREPARING SAME AND USE THEREOF
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,240
Score 221; DB 1; Length 32;
Pred. No. 2.67e-15;
1; Mismatches 1; Indels
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Pred. No. 9.59e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PILING DATE: 24: JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 994,084
FILING DATE: 16-DEC-1992
APPLICATION NUMBER: 992
                                                                                                                                                                                                      30 AA
                                                                                                      6 TAPRSLRRSSCFGGRMDRIGAQSGLGCNSFRY 37
                                                                                 1 TAPRSLRRSSCFGGRIDRIRAQSGLGCNSFRY 32
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LENGTH: 28
SEQUENCE 30 AA; 3303 MW; 4581 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 18 NOV-1991
APPLICATION NUMBER: 401,401
FILING DATE: 01.5EP-1989
APPLICATION NUMBER: 100,144
FILING DATE: 28-AUG-1987
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Best Local Similarity 100.0%;
Matches 28; Conservative
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Wed Jun 16 12:48:57 1999; MasPar time 4.75 Seconds 311.884 Million cell updates/sec

311.884 Million c Tabular output not generated.

Title: >VANDER-027-213.PEP
Description: (1-37) from vander027777.pep
Perfect Score: 279
Sequence: 1 LRALLTAPRSLRRSSCFGGRMDRIGAQSGLGCNSFRY 37

Scoring table: PAM 150 Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries Database: pir60 1:pir1 2:pir2 3:pir3 4:pir4 Statistics: Mean 32.756; Variance 52.653; scale 0.622

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Pred. No.	3.82e-45	3.82e-45	2.01e-44	2.01e-44	2.01e-44	5.49e-43	2.86e-43	1.49e-4]	1.49e-4]	3.45e-31	2.37e-2(2.85e-2(1.25e-1	5.61e-17	5.61e-17	1.52e-1(5.70e-14	1.87e-1	4.83e-1	3.19e-1(5.10e-1(8.29e-09	1.31e-08
	Description	natriuretic peptide A	atrial natriuretic pe	atrial natriuretic fa	atrial natriuretic pe	hypothetical natriure	atrial natriuretic pe	atrial natriuretic fa	aldosterone secretion	brain natriuretic pep	brain natriuretic fac	brain natriuretic pep	alpha-atrial natriure	ventricular natriuret	natriuretic peptide B	brain natriuretic pep	atrial natriuretic fa	brain natriuretic fac	lebetin 2 isoform bet					
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	Match Length DB	151	152	149	150	153	153	128	152	152	161	145	30	103	131	131	105	140	36	134	27	27	121	37
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lebetin 2 isoform alp	peptide t	peptide t	peptide C	peptide c	brain natriuretic pep	natriuretic peptide C	natriuretic peptide t	type-B natriuretic pe	brain natriuretic pep	3-type natriuretic pe		c-type natriuretic pe	brain natriuretic pep	natriuretic peptide,	protein	protein	qlucosamine - fructose	polysulfide reductase	cetracycline resistan	receptor tyrosine kin	protein-tyrosine kina
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24	22	56	27	28	53	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

ALTERNATE NAMES ARRIVETICE DEPLICATION - human natriuretic peptide A precursor - human prepronatrical natriuretic factor; atrial natriuretic peptide A precursor atrial appearant organical natriuretic factor; atrial appearant prepronatricalization (PND) atrial alpha natriuretic factor; arrial agamman natriuretic factor; arrial appearant and the proper factor; arrial arrial arrial and the proper factor; arrial arria
ferences GB: A29370 Seidman, C. Seidman, Science (19 Nucleotide natriured B29370

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123-150 ##label ONG
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Best Local Similarity 100.0%;
Matches 37; Conservative
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                                                                                                       ##molecule_type DNA
##residues 26-1
                                                                                                                                                                                        natriuretic.
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CLASSIFICATION
KEYWORDS
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REFERENCE
#authors
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124-151
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                                                                    #authors Kangawa, K.; Matsuo, H.
#journal Blochem. Blophys. Res. Commun. (1984) 118:131-139
#title Purification and complete amino acid sequence of alpha-human acrass-references MID:84128019
#accession A32733
                                                                                                                                                                                                                                                                   Nakayama, K.; Ohkubo, H.; Hirose, T.; Inayama, S.; Nakanishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #authors Maki, M.; Parmentier, M.; Inagami, T.
#journal Blochem. Blophys. Res. Commun. (1984) 125:797-802
#ille Cloning of genomic DNA for human atrial natriuretic factor.
#cross-references MuID:85096983
                                                                                                                                                                                                                                                                                                      Nature (1984) 310:699-701
mRNA sequence for human cardiodilatin-atrial natriuretic
factor precursor and regulation of precursor mRNA in rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #authors Vanneste, Y.; Michel, A.; Deschodt-Lanckman, M.
#journal Eur. J Blochem. (1991) 196:281-286
#title Hydrolysis of intact and Cys-Phe-cleaved human atrial
natriuretic peptide in vitro by human tissue kallikrein.
#cross-references MUID:9117698
#accession 514097
##nolecule_type protein
##residues natural and synthetic peptide sujected to kallikrein
##note proteolysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               # Bauthors 21vin. R.A.; Condra, J.H.; Dixon, R.A.; Seidah, N.C.; Chretien, M.; Nemer, M.; Chamberland, M.; Drouin, J. Chretien, M.; Nemer, M.; Chamberland, M.; Drouin, J. Proc. Natl. Acad. Sci. U.S.A. (1984) 81:6325-6329 Molecular cloning and characterization of DNA sequences encoding rat and human atrial natriuretic factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypertension (1985) 7:31-34 Molecular studies of the atrial natriuretic factor gene.
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##msidecule_type mRNA
##msideus
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##cross-references GB:K02044; NID:g178631; PID:g178632
:NCE 139459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##residues 1-64,'D',66-151 ##label RE4 ##cross-references GB:M54951; NID:g178636; PID:g178638
                                                                                                                                                                                                                                                                                                                                                                                                                                               ##residues 1-151 ##label RES
##cross-references GB:M30262; NID:g180181; PID:g180182
NNCE S14097
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##cross-references GB:K02043
NCE A32733
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Nature (1984) 312:656-658
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                                                                                                                                                                                                     ##molecule_type protein
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#domain signal sequence #status predicted #label SIG\
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#product alpha atrial natriuretic peptide #status
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##residues
##residues
1-15; ##label VLA
##cross-references GB:M13145; NID:g162665; PID:g162666
ERBNCE Ago, H.; McNicoll, N.; Lazure, C.; Seidah, N.; Chretien;
#authors Cantin, M.; De Lean, A.
#journal Life Sci. (1986) 38:1309-1315
#fitle Purification and sequence determination of bovine atrial
#cross-references MUID:86173941
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ANP: atrial natriuretto polypeptide
#formal_name Bos primigenius taurus #common_name cattle
30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change
20-Mar-1998
A90124; A93049; A24247; A26090
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#journal Biochem. Blophys. Res. Commun. (1986) 136:396-403
#title Structure and analysis of the bovine atrial natriuretic peptide precursor gene.
#cross_references_MUID:86215205
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#title Nucleotide sequence of the gene encoding human atrial natriuretic factor precursor.
#cross-references MUID:85061627
#accession 137167
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#length 151 #molecular-weight 16395 #checksum 3644
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experimental #label ANP\
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##cross-references EMBL:X01471; NID:928690
T Cardiodilantin is a vasoconstrictor but
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##cross-references GDB:118727; OMIM:108780
#map_position 1p36-1p36
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Nucleic Acids Res. (1990) 18:6704
Nuclectide sequence of a porcine prepro atrial natriuretic
peptide (ANP) cDNA.
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alpha atrial natriuretic peptide; gamma atrial natriuretic
factor (cardiodilatin)
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predicted #label ANF\
#product alpha atrial natriuretic peptide #status
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21-Nov-1993 #sequence_revision 14-Jul-1994 #text_change
20-Mar-1998
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ANP; atrial natriuretic polypeptide
#formal_name Canis lupus.familiaris #common_name dog
31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change
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#molecular-weight 16518 #checksum 7552
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Biochem. Biophys. Res. Commun. (1985) 132:892-899
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##cross-references EMBL:X54669; NID:g1883; PID:g1884
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|th 149  #molecular-weight 15819 #
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Pred. No. 2.01e-44;
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Pred. No. 3.82e-45;
0; Mismatches 0;
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##residues 1-149 ##label OIK
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#accession A25302
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Best Local Similarity 97.3%;
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Best Local Similarity 100.0%;
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ANP; atrial natriuretic polypeptide
#formal_name Oryctolagus cuniculus #common_name domestic
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31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change
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#product gamma atrial natriuretic factor #status
predicted #label ANF\
product alpha atrial natriuretic peptide #status
product alpha atrial natriuretic peptide #status
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#th 150 #molecular-weight 16351 #checksum 9859
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FICATION #superfamily natriuretic peptide A precursor
Y #length 153 #molecular-weight 16825 #checksum 960
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Blochem. Blophys. Res. Commun. (1985) 132:892-899
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Carlquist, M.; Mutt, V.
Anat. Embryol. (1983) 168:307-313
The right auricle of the heart is an endocrine cardiodilatin as a peptide hormone candidate.
A60899
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Schulz-Knappe, P.; Forssmann, W.G.
submitted to the EMBL Data Library, March 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 276; DB 1; Le. Pred. No. 2.01e-44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 LRALLAAPRSLRRSSCFGGRMDRIGAQSGLGCNSFRY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1-153 ##label MAE
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#accession B25302
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                                                                                                                                                                                                                                                                                                                                                                                                                                           98.9%;
larity 97.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 98.9%;
Local Similarity 97.3%;
nes 36; Conservative
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B25302
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                                                                                                                                    ##molecule_type protein
                                                                                                                                                                                                                                                                                                                                                                                                 #length 150
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##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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the rat atrial

130-146

124-151 26-151

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Atlas, S.A.; Kleinert, H.D.; Camargo, M.J.; Januszewicz, A.; Sealey, J.E.; Laragh, J.H.; Schilling, J.W.; Lewickl, J.A.; Johnson, L.K.; Mack, T. Nature (1984) 309:717-719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #authors Maki, M.; Takayanagi, R.; Misono, K.S.; Pandey, K.N.;

#journal Tibbetts, C.; Inagami, T.

#journal Nature (1984) 309:722-724

#title Structure of rat arrial natriuretic factor precursor deduced from CDNA sequence.

#cross-references MUID:84219798

#accession A93332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #authors Currie, M.G.; Geller, D.M.; Cole, B.R.; Siegel, N.R.; Fok, K.F.; Adams, S.P.; Eubanks, S.R.; Galluppi, G.R.; Needleman, P. Needleman, P. Science (1984) 223:67-69 #title Purification and sequence analysis of bloactive atrial peptides (atriopeptins).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #authors Seidman, C.E.; Duby, A.D.; Choi, E.; Graham, R.M.; Haber, Homcy, C.; Smith, J.A.; Seidman, J.G.
#journal Science (1984) 225:324-326
#title The structure of rat preproatrial natriuretic factor as defined by a complementary DNA clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thibault, G.; Murthy, K.K.; Gutkowska, J.; Seidah, N.G.;
Lazure, C.; Chretien, M.; Cantin, M.
Peptides (1988) 9:47-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##molecule_type mRNA
##residues 1-152 ##label SEI
##cross-references GB:K02062; GB:K02063; NID:g202899; PID:g202900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##residues 1-152 ##label MAK
##cross-references GB:X00665; EMBL:X00658; NID:955711; PID:955712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *title Purification, sequencing and synthesis of natriuretic vasoactive rat atrial peptide. **eferences MUID:84219796
                                                                                                                                 #authors A93331
#authors Yamanaka, M.; Greenberg, B.; Johnson, L.; Seilhamer, Brewer, M.; Friedemann, T.; Miller, J.; Atlas, S.; J.; Erotaka, J.; Friedes, J.
#journal Nature (1984) 309:719-722
#Litle Cloning and sequence analysis of the cDNA for the rat natriuretic factor precursor.
#cross_references MUID:84219797
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                                              ##molecule_type DNA
##residues 1-152 ##label ARG
##cross-references GB:K02062; NID:9202899; PID:9202900
                                                                                                                                                                                                                                                                                                                                                                                                                 ##residues 1-152 ##label YAM
##cross-references EMBL:X00665; NID:955711; PID:955712
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##residues 126-149 ##label ATL
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##residues 127-149 ##label CUR
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#accession PT0061
##molecule_type protein
cross-references MUID:85182558
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                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             atrial natriuretic peptide precursor - guinea pig (fragment)
#formal_name Cavia porcellus #common_name guinea pig
20-Feb-1995 #sequence_revision 30-Jan-1998 #text_change
20-Mar-1998
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#product atrial natriuretic peptide #status predicted
#label MAT\
#disulfide_bonds #status predicted
#length 128 #checksum 8741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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atrial natriuretic factor precursor - rat
arrial natriuretic factor 33); ANF(8-33); ANF(8-33); atrial
natriuretic peptide; atriopeptin I; atriopeptin II;
auriculin A; auriculin B; preprocardionattin
#formal_name Rattus noirvegicus #common_name Norway rat
19-Feb-1984 #sequence_revision 15-Nov-1984 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##residues 1-128 ##label MAE ##cross-references EMBL.X58562; NID:g49543; PID:g49544 ##experimental_source heart atria; adult CLASSIFICATION #superfamily natriuretic peptide A precursor KEWWORDS atrium; diuretic; hormone; natriuretic; osmoregulation FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A01425; A93332; A43617; A93330; A94275; PT0061;
                    ##residues______1-153 ##label OIK
##cross_references GB:M12016; NID:g164770; PID:g164771
##superfamily natriuretic peptide A precursor
BS atrium; duuretic; hormone; natriuretic; osmoregulation
DS
                                                                                                                                                        #domain signal sequence #status predicted #label 
#product gamma atrial natriuretic factor #status
predicted #label ANF\
#product alpha atrial natriuretic peptide #status
predicted #label ANF\
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                                                                                                                                                                                                                                                                                                   #disulfide_bonds #status predicted
#length 153 #molecular-weight 16843 #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schulz-Knappe, P.; Forssmann, W.G.
submitted to the EMBL Data Library, March 1991
S14872
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Pred. No. 2.86e-42;
                                                                                                                                                                                                                                                                                                                                                                                       Length 153;
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J. Biol. Chem. (1985) 260:4568-4571
The gene for rat atrial natriuretic factor.
                                                                                                                                                                                                                                                                                                                                                                                 Score 270; DB 1; Le
Pred. No. 5.49e-43;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
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Best Local Similarity 94.6%;
Matches 35; Conservative
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Best Local Similarity 97.3%;
Matches 36; Conservative
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##molecule_type mRNA
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                                                                             CLASSIFICATION
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#authors

105-121

SUMMARY

99-128

ACCESSIONS

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REFERENCE

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Seidah, N.G.; Lazure, C.; Chretien, M.; Thibault, G.; Garcia,
R.; Cantin, M.; Genest, J.; Nutt, R.F.; Brady, S.F.; Lyle,
T.A.; Paleveda, W.J.; Colton, C.D.; Ciccarone, T.M.; Veber,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lowicki, J.A.

Ilournal Proc. Natl. Acad. Sci. U.S.A. (1987) 84:2175-2179

#fitle Identification of atrial natriuretic factor gene transcripts in the central nervous system of the rat.

#cross-references MUID:87175636
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##cross-references GB:#Z1498; NID:92020905; PID:9202908

A disulfide bond is required for full activity of atriopeptins.

T Several active peptides may be derived from the carboxyl region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##molecule_type mRNA
##residues 1-152 ##label FLY
##cross-references GB:K02062; NID:g202899; PID:g202900
##cross-references GB:K02062; NID:g202899; PID:g202900
##note part of this sequence, including the amino ends of thre
mature peptides, was confirmed by protein sequencing
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#fitle Identification of rat gamma atrial natriuretic polypeptide
and characterization of the cDNA encoding its precursor.
#cross-references WUID:85061500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Belcourt, D.; Varma, D.R.; Toney, K.; Bennett, H.P.J.
Protein Expr. Purif. (1990) 1:28-32
Purification of rat pro-atrial natriuretic factor: a
simplified scheme using reversed-phase high-performance
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Sakuragawa, Y.; Nakazato, H.; Fukuda, A.; Minamino, N.;
Matsuo, H.
                                                                                                                                                                                                                                                                                                                                          Flynn, T.G.; Davies, P.L.; Kennedy, B.P.; de Bold, M.L.;
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#Journal Can. J. Physiol. Pharmacol. (1987) 65:2013-2020
#title the elucidation of the structure of atrial natriuretic
#cross-references MUID:88109092
                                                                                                           #journal Proc. Natl. Acad. Sci. U.S.A. (1984) 81:2640-2644
#fittle Amino acid sequence of homologous rat atrial peptides:
natriuretic activity of native and synthetic forms.
#cross-references MUID:84194062
                                                                                                                                                                                                                                                                                                                                                                                                                             #title Alignment of rat cardionatrin sequences with the preprocardionatrin sequence from complementary DNA. #cross-references MUID:85168263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preliminary; translated from GB/EMBL/DDBJ
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NCE 158057
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NCE 152678
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Science (1985) 228:323-325
                                                                                                                                                                                                                                                                                    118-150 ##label SE2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      liquid chromatography.
*cross-references MUID:93044510
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##residues 25-39 ##label BEL
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*product ANF(1-33) *status experimental *label ANF1\
*product ANF(2-33) *status experimental *label ANF3\
*product ANF(3-33) *status experimental *label ANF3\
*product Cardionatrin I *status experimental *label CNI\
*product ANF(8-33) *status experimental *label ANF4\
*product ANF(8-33) *status experimental *label ANF4\
*product auriculin B *status experimental *label ANB\
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#disulfide_bonds #status experimental
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predicted #label ANP\
#disulfide_bonds #status predicted
#length 152 #molecular-weight 16645 #checksum 9384
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Seidman, C.E.; Bloch, K.D.; Klein, K.A.; Smith,
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Pred. No. 1.49e-41;
Mismatches 0;
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Pred. No. 1.49e-41;
3; Mismatches 0;
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Science (1984) 226:1206-1209
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Best Local Similarity 91.9%;
Matches 34; Conservative
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H:; de Lean, A.
Endocrinology (1989) 124:1591-1593
Aldosterone secretion inhibitory factor: a novel neuropeptide
in bovine chromaffin cells.
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Mol. Endocrinol. (1989) 3:1823-1829
Purification and primary structure of pro-aldosterone
secretion inhibitory factor from bovine adrenal chromaffin
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                                                                                                                                                                                                                                                                                 atriopeptin
#formal_name Rana ridibunda #common_name laughing frog
01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change
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                                                                                                                                                                                                                                             #length 145 #molecular-weight 15934 #checksum 1892
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                                                                                                                                                                                                                                                                                                                                                                                                     Lazure, C.; Ong, H.; McNicoll, N.; Netchitailo,
M.; de Lean, A.; Vaudry, H.
FEBS Lett. (1988) 238:300-306
                                       Length 145
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from Fig. 3 in lacking residues 3.6
#superfami.y natriuretic peptide A precursor
#length 30 #checksum 4650
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                                                                                                                       109 LRELLNAPRSMRRSSDCFGSRIDRIGAGSGMGCGR-RF 145
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                                       Score 199; DB 2;
Pred: No. 2.37e-26;
                                                                                                                                            1 LRALLTAPRSLRRSS-CFGGRMDRIGAQSGLGCNSFRY 37
                                                                             5; Mismatches
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##residues 1-30 ##label LAZ
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#accession S01657
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#accession A30976
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Best Local Similarity 76.7%;
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A41403
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Best Local Similarity 71.1%;
Matches 27; Conservative
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                                                                           155480 #type complete hypothetical natriuretic peptide/phage fr coat protein mutant fusion protein - synthetic
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ANP; atrial natriuretic factor (ANF)
atrial natriuretic peptide-21; atrial natriuretic peptide-24
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                                                                                                                                                                                                                                                                                                  S.; Baumanis, V. 1. Changary, M.; Garmanis, V. 1. Biotechnol. (1993) 30:231-243
J. Biotechnol. (1993) 30:231-243
High level expression of alpha-human atrial natriuretic factor as a fusion polypeptide with phage fr coat protein in Escherichia coll.
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Biochem. Biophys. Res. Commun. (1988) 155:1338-1345
Identification of new atrial natriuretic peptides in frog
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expressed in Escherichia coli
02-Jul-1996 *sequence_revision 05-Sep-1996 *text_change
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##residues 122-145 ##label SAK
VT In mammals, several active peptides may be derived from the
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Pproduct atrial natifuretic peptide-24 #status
experimental #label M24\
#product atrial natriuretic peptide-21 #status
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1; Mismatches 0; Indels
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#length 161 #molecular-weight 17287
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Best Local Similarity 96.6%;
Matches 28; Conservative
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Hournal Biochem Biophys. Res. Commun. (1988) 157:402-409

Hitle Isolation and identification of a high molecular weight brain natriuretic peptide in porcine cardiac atrium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Porter, J.G.; Arfsten, A.; Palisi, T.; Scarborough, R.M.; Lewicki, J.A.; Sellhamer, J.J.
J. Biol. Chem. (1989) 264:6689-6692
Cloning of a CDNA encoding porcine brain natriuretic peptide.
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brain natriuretic peptide precursor - pig
#formal_name Sus scrofa domestica #common_name domestic pig
27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change
29-Jan-1999
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#journal Blochem. Blophys. Res. Commun. (1988) 157:410-416

#litle Cloning and sequence analysis of cDNA encoding a precursor for porcine brain natriuretic peptide.

#cross-references MUID:89061744
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#length 103 #molecular-weight 11249 #checksum 7671
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##cross-references GB:M25547; GB:J04708; GB:M22477; GB:M22478;
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Pred. No. 5.61e-17;
10; Mismatches 5; Indels
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Sudoh, T.; Minamino, N.; Kangawa, K.; Matsuo,
                                                                Score 160; DB 2; Length 103
Pred, No. 1.25e-17;
7; Mismatches 6; Indels
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brain natriuretic factor 32
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#cross-references MUID:89214071
#accession A33873
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larity 60.5%;
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       SUMMARY
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'n
                                                                                                                                                                                                                                                                                                #domain signal sequence #status predicted #label SIG\
#product brain gamma natriuretic factor #status
predicted #label GAM\
Biochem. Biophys. Res. Commun. (1988) 155:726-732
Brain natriuretic peptide-32: N-terminal six amino acid
extended form of brain natriuretic peptide identified in
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                                                                                                                              Length 131;
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                                                                                                                                                                                                                                 106-131 ##label SU2
#Superfamily natriuretic peptide A precursor
brain; natriuretic
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 157; DB 2; Pred. No. 5.61e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95 LRGI-RSPKTMRDSGCFGRRLDRIGSLSGLGCNVLRRY 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Mismatches
                                                                                          ##molecule_type protein
##residues 100-131 ##label SUD
                                                                *cross-references MUID:88339957
                                                                                                                                                                                                                                                                                                                                                                                                                               56.3%;
ilarity 55.3%;
Conservative
                                                porcine brain
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Best Local Similarity 5
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed Jun 16 12:49:46 1999; MasPar time 3.22 Seconds 324.910 Million cell updates/sec Run on:

Tabular output not generated.

>VANDER-027-213.PEP (1-37) from vander027777.pep 279 Description: Perfect Score:

1 LRALLTAPRSLRRSSCFGGRMDRIGAOSGLGCNSFRY 37 Seguence:

PAM 150 Gap 11 Scoring table:

77977 seqs, 28268293 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

swiss-prot37 1:swissprot Database:

Mean 33.663; Variance 47.480; scale 0.709 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ			SUMMANTES	. •	
Result No.	Score	Query Match	Query Match Length DB	DB	DI.	Description	Pred. No.
-	279	100.0	152	-	ANF_BOVIN	ATRIAL NATRIURETIC FAC	2.07e-51
~	279	100.0	153	Н	ANF_HUMAN	ATRIAL NATRIURETIC FAC	2.07e-51
m	276	98.9	149	Н	ANF_CANFA	ATRIAL NATRIURETIC FAC	1.36e-50
4	276	98.9	150		ANF_PIG	ATRIAL NATRIURETIC FAC	1.36e-50
S	276	98.9	153	٦	ANF_HORSE	ATRIAL NATRIURETIC FAC	1.36e-50
9	270	96.8	153	٦	ANF_RABIT	ATRIAL NATRIURETIC FAC	5.80e-49
7	267	95.7	128	-	ANF_CAVPO	ATRIAL NATRIURETIC FAC	3.77e-48
80	264	94.6	152	٦	ANF_RAT	ATRIAL NATRIURETIC FAC	7
σ	264	94.6	152	٦	ANF_MOUSE	ATRIAL NATRIURETIC FAC	2.45e-47
10	199	71.3	145	٦	ANF_RANCA	ATRIAL NATRIURETIC FAC	4
11	172	61.6	30	-	ANF_RANRI	ATRIAL NATRIURETIC FAC	m.
12	160	57.3	103	-	ANFB_BOVIN	BRAIN NATRIURETIC PEPT	m.
13	157	56.3	131	٦	ANFB_PIG	BRAIN NATRIURETIC PEPT	ä
14	155	. 55 . 6	140	٦	ANFB_CANFA	BRAIN NATRIURETIC PEPT	5.09e-19
15	143	51.3	140	٦	ANF_CHICK	ATRIAL NATRIURETIC FAC	4
16	131	.47.0	36	٦	ANFV_ANGJA	VENTRICULAR NATRIURETI	2.79e-13
17	129	46.2	134	_	ANFB_HUMAN	BRAIN NATRIURETIC PEPT	8.16e-13
18	124	44.4	27	٦	ANF_ANGJA	ATRIAL NATRIURETIC FAC	Ä
19	118	42.3	121	٦	ANFB_RAT	BRAIN NATRIURETIC PEPT	2.67e-10
20	114	40.9	22	٦	ANFC_CHICK	C-TYPE NATRIURETIC PEP	2.10e-09
21	112	40.1	131	٦	ANFC_ANGJA	C-TYPE NATRIURETIC PEP	5.81e-09
22	107	38.4	115	٦	ANFC_TRISC	C-TYPE NATRIURETIC PEP	
23	107	38.4	115	-	ANFC_SCYCA	C-TYPE NATRIURETIC PEP	7.21e-08

7.21e-08 7.21e-08 7.21e-08 7.21e-08 7.21e-08 7.21e-08 7.21e-08 7.21e-08 7.21e-08 8.32e-07 8.53e-07 5.23e-02 5.23e-02 5.23e-02	1.38e+00 1.38e+00 1.38e+00 1.38e+00 2.04e+00 2.04e+00
C-TYPE NATRIURETIC PEP C-TYPE TETRACYCLINE REDUCTASE TETRACYCLINE RESISTANC EPHRIN TYPE-A RECEPTOR SERKING-THREONINE-PROTE SERKING-THREONINE-PROTE	CYSTEINE SYNTHASE CHLO HYPOTHETICAL 46.5 KD P IDURONATE 2-SULFATASE ELONGATION FACTOR 6 I PROBABLE RNA-DIRECTED PROBABLE RNA-DIRECTED
ANFC_RAT ANFC_PIG ANFC_SHEEP ANFC_GHUMA ANFC_MOUSE ANFC_MOUSE ANFD_RANCA BOND_DENAN FORM_MOLSU EPAI_HUMAN KRI_HSVII	CYSL_SPIOL YK33_YEAST IDS_HUMAN EFG1_TREPA V2A_CMVY V2A_CMVY
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ALIGNMENTS

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Molecular cloning and characterization of DNA sequences encoding rat
                                                                                                                                                                                                  SEQUENCE OF 124-151.
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130
152
153 AA;
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DISULFID
VARIANT
SEQUENCE
                                                                                                 MEDLINE;
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13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MINISTER, C. IMAI M., UENO A., TANAKA S., NOGUCHI T., NAKAZATO H., KANDAWA K., FUKUDA A., MATSUO H.;
"Cloning and sequence analysis of cDNA encoding a precursor for human atrial natriuretic polypeptide.";
NATURE 309:724-726(1984).
                ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleotide sequence of the gene encoding human atrial natriuretic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 84295577.
NAKAYAMA K., OHKUBO H., HIROSE T., INAYAMA S., NAKANISHI S.;
"MRNA sequence for human cardiodilatin-atrial natriuretic factor
precursor and regulation of precursor mRNA in rat atria.";
NATURE 310:699-701(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIVIN R.A., CONDRA J.H., DIXON R.A.F., SEIDAH N.G., CHRETIEN M., NEMER M., CHAMBERLAND M., DROUIN J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EIDMAN C.E., BLOCH K.D., KLEIN K.A., SMITH J.A., SEIDMAN J.G.; Nucleotide sequences of the human and mouse atrial natriuretic
                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEMER M., CHAMBERLAND M., SIROIS D., ARGENTIN S., DROUIN J. DIXON R.A.F., ZIVIN R.A., CONDRA J.H.;

"Gene structure of human cardiac hormone precursor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 85061627.
GREENBERG B.D., BENCEN G.H., SEILHAMER J.J., LEWICKI J.A.,
                                                                                               Length 152;
                                                                                         Score 279; DB 1; Length 152
Pred. No. 2.07e-51;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBMITTED (MAY-1998) TO EMBL/GENBANK/DDBJ DATA BANKS
              123 150 ATRIAL NATRIURETI
129 145
152 Aa; 16518 MW; CF200882 CRC32;
                                                                                                                                                                         114 LRALLTAPRSLRRSSCFGGRMDRIGAQSGLGCNSFRY 150
                                                                                                                                                                                              153
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                                                                                                                                                                                                                                                                                                                                                                                                                     (ANP) (PREPRONATRIODILATIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           factor genes.";
SCIENCE 226:1206-1209(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-151 FROM N.A. MEDLINE; 84219799.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-151 FROM N.A. MEDLINE; 85061626.
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                                                                                           Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 37; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      factor precursor.";
NATURE 312:656-658(1984).
                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             HOMO SAPIENS (HUMAN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85065766
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P01160;
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SEIDMAN C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ERRINGTON
              PEPTIDE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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ng as its content is in no
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-!- SIMILARITY: BELGN'SS TO THE NATRIURETIC PEPTIDES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 94318633.

PAIRBROTHER, W.J., MCDOWELL R.S., CUNNINGHAM B.C.;

"Solution conformation of artial natriuretic peptide variant
selective for the type A receptor.";

BIOCHEMISTRY 33:8897-3904(1994).

- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE
SUBSTRACE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
C24A68AF CRC32;
C24A68AF CRC32;
                                                                                                                                                                                                                                                                                                                               MEDLINE; 84128019.
RANGAWA K., MATSUO H.,
Purification and complete amino acid sequence of alpha-human atrial
natriuretic polypeptide (alpha-hANP).";
BIOCHEM. BIOPHYS. RES. COMMUN. 118:131-139(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -! - THE HUMAN GENOME CONTAINS 2 DIFFERENT PREPRONATRIODILATIN GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARDIODILATIN-RELATED PEPTIDE (CDP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRUCTURE BY NMR OF 124-151 MUTANT SELECTIVE FOR NPR-C RECEPTOR
                                                                                                                                                          MAKI M., PARMENTIER M., INAGAMI T.;
"Cloning of genomic DNA for human atrial natriuretic factor.";
BIOCHEM. BIOPHYS. RES. COMMUN. 125:797-802(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Pred. No. 2.07e-51;
0; Mismatches 0; Indels
and human atrial natriuretic factors.";
PROC. NATL. ACAD. SCI. U.S.A. 81:6325-6329(1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 LRALLTAPRSLRRSSCFGGRMDRIGAQSGLGCNSFRY 151
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PFAM; PF00212; ANP; 1.
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K02043; G178630;
X01471; E27452; ALT_SEQ.
K02044; G178632;
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Best Local Similarity 100.0%;
Matches 37; Conservative
                                                                                           1-75 FROM N.A.
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146
153
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PIR; A22693; A22693.
PIR; A32733; A32733.
PDB; 1ANP; 07-APR-95.
MIM; 108780; -.
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01-AUG-1992
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P27104;
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                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
(ANP) (PREPRONATRIODILATIN).
                                              01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
                                                                                                                                                                                                                                                ď
                                                                                                                                                                 MEDLINE; 86076557.

OIKAWA S., IMAI M., INUZUKA C., TAWARAGI Y., NAKAZATO H., MATSUO H.;

*Structure of dog and rabbit precursors of atrial natriuretic
polypeptides deduced from nucleotide sequence of cloned CDNA.";

BIOCHEM. BIOPHYS. RES. COMMUN. 132:892-899(1985).

-!- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE
SUBSTANCE SYNTHESIZED IN MAMMALIAN AFRIA AND IS THOUGHT TO PLAY A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE, 91067478.
MARGERT H.J., APPELHANS H., GASSEN H.G., FORSSMANN W.G.;
"Nucleotide sequence of a porcine prepro atrial natriuretic peptide (ANP) conna.".
NUCLEIC ACIDS RES. 18:6704-6704(1990).
                                                                                                                                                                                                                                                                                   A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS. SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
                                                                                                                                                                                                                                                          KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUKARYOTA; METAŽOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
ARTIODACTYLA; SUIFORMES; SUINA; SUIDAB; SUS.
                                                                                                                    EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
CARNIVORA; FISSIPEDIA; CANIDAE; CANIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 276; DB 1; Length 149;
Pred. No. 1.36e-50;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 LRALLAAPRSLRRSSCFGGRMDRIGAQSGLGCNSFRY 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15819 MW; D4F3A6CF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LRALLTAPRSLRRSSCFGGRWDRIGAQSGLGCNSFRY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          150 AA.
          149 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1. PFAM; PF00212; ANP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-1992 (REL. 21, CREATED)
                                  07, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.9%;
llarity 97.3%;
Conservative
                                                                                  (ANP) (PREPRONATRIODILATIN)
                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M12045; G163901; -.
           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149
                                                                                                           CANIS FAMILIARIS (DOG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 36; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VASOACTIVE; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149 AA;
                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUS SCROFA (PIG)
                                   01-APR-1988
        CANFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JT 4
ANF_PIG
P24259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
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01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAEGERT H.J., RICHTER R., SCHMAEDING G., FORSSMANN W.G.;
SUBMITTED (MAR.1991) TO EMBL/GENBANK/DBJ DATA BANKS.
-1- FUNCTION: ATRIAL NATRIURELIC FACTOR (ANF) IS A POTENT VASOACTIVE
SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
                                                                                                                      METZ J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BY SIMILARITY).
ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
                                                                                                                                                                                                                                                                             CELL TISSUE RES. 238:425-430(1984).
-1- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE SUBSTANCE SYNTHESIZED IN NAMMALIAN ATRIA AND IS THOUGHT TO PLAY REY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS.
-1- SIMILARIȚY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
                                                                                                                                                                                     heart constitute an endocrine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARDIODILATIN-RELATED PEPTIDE (CDP)
                                                 MEDLINE; 85124561.
FORSEMANN W.G., BIRR C., CARLQUIST M., CHRISTMANN M., FINKE R., FORSEMANN W.G., BIRR C., CARLQUIST M., CHRISTMANN M., FINKE R., ME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                   HENSCHEN A., HOCK D., KIRCHHEIM H., KREYE V., LOTTSPEICH F., MUTT V., REINECKE M.;

"The auricular myocardiocytes of the heart constitute an endo organ. Characterization of a porcine cardiac peptide hormone, cardiodilatin-126.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PERISSODACTYLA; EQUIDAE; EQUIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 150;
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Pred. No. 1.36e-50;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
4FF67B94 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 LRALLAAPRSLRRSSCFGGRMDRIGAQSGLGCNSFRY 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LRALLTAPRSLRRSSCFGGRMDRIGAQSGLGCNSFRY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; S13107; S13107.
PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-ADAMITICUS; TISSUE-HEART ATRIUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16351 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ANP) (PREPRONATRIODILATIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                larity 97.3%;
Conservative
                             IISSUE-HEART RIGHT ATRIUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24
54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM; PF00212; ANP; 1. VASOACTIVE; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150 AA;
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tes 36; Conser
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SEQUENCE OF 25-150
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the European Bioinformatics Institute. There are no restrictions on its may by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OIKAWA S., IMAI M., INUZUKA C., TAWARAGI Y., NAKAZATO H., MATSUO H.; "Structure of dog and rabbit precursors of atrial natriuretic polypeptides deduced from nucleotide sequence of cloned cDNA."; BIOCHEM. BIOCHEM. 132.892.899(1985).

-:- FUNCTION: ATRIAL NATRIBETIC FACTOR (ANF) IS A POTENT VASOACTIVE SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
                                                                                                                                                                                                                                                                                                                          POTENTIAL.
ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
BY SIMILARITY.
: FESDSF4A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP)
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A DISULPIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS.
SIMILARITY: BELONGS TO THE NATRIURETIC PEPTINES FAMILY.
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EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
LAGOMORPHA; LEPORIDAE; ORYCTOLAGUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 153;
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Pred. No. 5.80e-49;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 276; DB 1; 1
Pred. No. 1.36e-50;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16843 MW; 1FA4FB42 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153. AA.
                                                                                                                                                                   EMBL; X58563; G1009; -.
PIR; S14873; S14873.
PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
PEM: PF00212; ANP; 1.
VASOACTIVE: SIGNAL.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; B25302; AWRB.
PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
PFAM; PF00212; ANP; 1.
VASGACTIVE; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                    153 AA; 16825 MW;
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ilarity 97.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 18.0%; Local Similarity 97.3%; Local Similarity 97.3%; Local Similarity 97.3%; Local Servative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity
Matches 36; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1988 (REL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANF_RABIT
P07500;
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                                                                                                                                                                                                                                        01-AUG-1992 (REL. 23, CREATED)
01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
ATRIAL NATRIURETIC FACTOR PRECUESOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
(ANP) (PREPRONATRIODILATIN) (FRAGMENT).
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ATRIAL NATRIORETIC PÉPTIDE, ALPHA (ANP).
BY SIMILASTIY.
2 Z22F52D CR32;
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SCHULZ-KNAPPE P., FORSSMANN W.G.;
SUBMITTED (MAR.1991) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: ATRIAL NATRIVERIC FACTOR (ANF) IS A POTENT VASOACTIVE
SUBSTANCE SYNTHESIZED IN WAMMALIAN ATRIA AND IS THOUGHT TO PLAY
KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
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EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; HYSTRICOGNATHI; CAVIIDAE; CAVIA.
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1; Mismatches 1
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115 LRALLTAPRSLRRSSCFGGRIDRIGAQSGLGCNSFRY 151
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LAST ANNOTATION UPDATE)
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE;
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PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
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128 AA; 13366 MW;
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21-JUL-1986 (REL. 01, LAST SEQU
15-DEC-1998 (REL. 37, LAST ANNC
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Matches 35; Conservative
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TISSUE-HEART ATRIUM;
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P27596;
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P01161;
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MEDLINE; 86038509.
ZIVIN R.A. CONDRA J.H., DIXON R.A.F., SEIDAH N.G., CHRETIEN M.,
NEMER M., CHAMBERLAND M., DROUIN J.;
"Molecular cloning and characterization of DNA sequences encoding rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 84219796.
ATLAS S.A., KLEINERT H.D., CAMARGO M.J., JANUSZEWICZ A., SEALEY J.E.,
LARAGH J.H., SCHILLING J.W., LEWICKI J.A., JOHNSON L.K., MAACK T.;
"Purification, sequencing and synthesis of natriuretic and vasoactive
rat atrial peptide.";
NATURE 309:717-719(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The elucidation of the structure of atrial natriuretic factor, a new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GARDNER D.G., VLASUK G.P., BAXTER J.D., FIDDES J.C., LEWICKI J.A.; "Identification of atrial natriaretic factor gene transcripts in the central nervous system of the rat."; PROC. NATL. ACAD. SCI. U.S.A. 84:2175-2179(1987).
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"The structure of rat preproatrial natriuretic factor as defined by a complementary DNA clone.";
SCIENCE 225:324-326(1984).
                                                                                                                                          NAGAMI T.; Structure of rat atrial natriuretic factor precursor deduced from
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            BREWER
                                                "Cloning and sequence analysis of the cDNA for the rat atrial natriuretic factor precursor.";
NATURE 309:719-722(1984).
         AMANAKA M., GREENBERG B., JOHNSON L., SEILHAMER J.J., BREWEI
RIEDEMANN T., MILLER J., ATLAS S.A., LARAGH J., LEWICKI J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 127-149, AND SYNTHESIS.
MEDLINE; 84097513.
CURRIE M.G., GELLER D.M., COLE B.R., SIEGEL N.R., FOK K.F.,
ADAMS S.P., EUBANKS S.R., GALLUPPI G.R., NEEDLEMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE: 8182158.
ARCENTIN S., NEMER M., DROUIN J., SCOTT G.K., KENNEDY B.P.,
DAVIES P.L.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and human atrial natriuretic factors.";
PROC. NATL. ACAD. SCI. U.S.A. 81:6325-6329(1984).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The gene for rat atrial natriuretic factor.";
J. BIOL. CHEM. 260:4568-4571(1985).
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SEQUENCE OF 38-152 FROM N.A.
MEDLINE; 87175636.
                                                                                                                                                                                NATURE 309:722-724(1984).
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84250178.
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84219798.
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13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
ATRIAL NATRIUMETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIUMETIC PEPTIDE)
(ANP) (PREPRONATRIODILATIN).
MIPPA OR PUD.
                                                                                                                             SEIDAH N.G., LAZURE C., CHRETIEN M., THIBAULT G., GARCIA R., CANTIN M., GENEST J., NUTT R.F., BRADY S.F., LYLE T.A., PALEVEDA W.J., COLTON C.D., CICCARONE T.M., VEBER D.F.; "Amino acid sequence of homologous rat atrial peptides: natriuretic
                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY AKEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
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Purification and sequence analysis of bioactive atrial peptides
                                                                                                                                                                                                                                                                                                                MEDLINE; 88203350.
THIBAULT G., MURTHY K.K., GUTKOWSKA J., SEIDAH N.G., LAZURE C.,
CHRETIEN M., CANTIN M.;
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Score 264; DB 1; Leng
NO. 2.45e-47;
                                                                                                                                                                                              "Amino acid sequence of homologous rat atrial pep
activity of mative and synthetic forms.";
PROC. NATL. ACAD. SCI. U.S.A. 81:2640-2644(1984).
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ATRIOPEPTIN I.
ATRIOPEPTIN II.
ATRIOPEPTIN III.
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PFAM; PF00212; ANP; 1.
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                       (atriopeptins).";
SCIENCE 223:67-69(1984).
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license elsement. (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANE_RANCA STANDARD; PRT; 145 AA.
P18909;
01-MAR-1992 (REL. 16, CREATED)
01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
                                                                                                                                                                                                                             TO PLAY A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RANA CATESBEIANA (BULL FROG).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
NEOBATRACHIA; RANOIDEA; RANIDAE; RANINAE; RANA.
                                                                                                                                                         factor genes.";
SCIENCE 226:1206-1209(1984).
-!- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE
SUBSTANCE SYNTHESIZED IN WAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SAKATA J., KANGAWA K., MATSUO H.;
"Identification of new atrial natiuretic peptides in frog heart.";
BICCHEM. BIOPHYS. RES. COMMUN. 155:1338-1345(1988).
-I- FUNCTION: VASOACTIVE ACTIVITY. HAS A CGMP-SIMULATING ACTIVITY.
-I- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
                                                                                                                                                                                                                                                                                            A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS. SIMILARITY: BELONGS TO THE NATRIORETIC PEPTIDES FAMILY.
                                                                                          MEDLINE; 85065766.
SEIDWAN C.E., BLOCH K.D., KLEIN K.A., SMITH J.A., SEIDWAN J.G.;
"Nucleotide sequences of the human and mouse atrial natriuretic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AURICULIN A (BY SIMILARITY).
AURICULIN B (BY SIMILARITY).
ATRIOPEPTIN I (BY SIMILARITY).
ATRIOPEPTIN II (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KOJIMA M.;
SUBMITTED (XXX-1992) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 2.45e-47;
3; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 LRALLAGPRSLRRSSCFGGRIDRIGAQSGLGCNSFRY 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y SIMILARITY.
5163CB23 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 264; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LRALLTAPRSI.RRSSCFGGRMDRIGAQSGLGCNSFRY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PSO0263; NATRIURETIC_PEPTIDE; 1.
PFAM; PF00212; ANP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16645 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94.6%;
ilarity 91.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; K02781; G387099; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A29370; AWMS.
MGD; MGI:97367; NPPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 122-145.
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127
127
129
129
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nes 34; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL.
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                                                                   SEQUENCE FROM N.A. MEDLINE; 85065766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-HEART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VASOACTIVE;
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DISULFID
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Matches
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between the Swiss Institute of Bioinformatics and the EMBL outstation its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
01-MAR-1989 (REL. 31, LAST ANNOTATION UPDATE)
ATRIAL NATRIURETIC FACTOR (ANF) (ATRIAL NATRIURETIC PEPTIDE) (ANP).
RANA RIDIBUNDA (LAGGHING FROG) (MARRA FROG).
EUKANYOTA: METAZOA: CHODATA: VERTEBRATA: AMPHIBIA; BATRACHIA: ANURA;
NEOBATRACHIA; RANOIDEA; RANIDAE; RANINAE; RANA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DE LEAN A., VAUDRY H.;

"The amino acid sequences of frog heart atrial natriuretic-like peptide and mammalian. ANF are closely related.";
FEES LETT. 238-300-36(61988).

-! FUNCTION: VASOACTIVE ACTIVITY. HAS A CGMP-STIMULATING ACTIVITY.

-! SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.

PROSITE: PS00263: NATRIURETIC_PEPTIDE; 1.

PRAM: PE00212: ANP: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANFB_BOVIN STANDARD; PRT; 103 AA.
P13204;
01-JAN-1990 (REL. 13, CREATED)
01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
BRAIN NATRIURETIC PEFTIDE PRECURSOR (BNP) (ALDOSTERONE SECRETION INHIBITORY FACTOR) (ASIF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
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MEDLINE; 89005705.
LAZURE C., ONG H., MCNICOLL N., NETCHITAILO P., CHRETIEN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                              ATRIAL NATRIURETIC FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 172; DB 1; Le
Pred. No. 3.12e-23;
4; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 LRELLNAPRSMRRSSDCFGSRIDRIGAQSGMGCGR-RF 145
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 199; DB 1;
Pred. No. 4.13e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LRALLTAPRSLRRSS-CFGGRWDRIGAQSGLGCNSFRY 37
                                                                                                                                                                                                                                                                                                                                                                                              15934 MW; 6A1FA352 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 AA; 3263 MW; 14A325F7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 AA
                                                                                                                                                                                                                                               PS00263; NATRIURETIC_PEPTIDE; 1
                                                                                                                                                                                                                                                                                                                         POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 APRSLRRSS-CFGGRNDRIGAQSGLGCNSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                            71.3%;
llarity 71.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.6%;
76.7%;
                                                                                                                                                                           EMBL; D01043; D1001314; -.
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Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                         23
145
141
                                                                                                                                                                                                                                                                         PFAM; PF00212; ANP; ... VASOACTIVE; SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity '
                                                                                                                                                                                                                                                                                                                                              122
125
145 AA;
                                                                                                                                                                                                 PIR; A31510; A31510.
PIR; JQ0947; JQ0947.
PROSITE; PS00263; NA
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BIOPHYS. RES. COMMUN. 157:402-409(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 1
100 1
106 1
109 1
26 131 AA;
                                                                                                                                  SEQUENCE OF 106-131.
                             OF 100-131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A31517; A31517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 92007873.
                                                                                                                                                   88156915.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00212;
VASOACTIVE; BR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .21;
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BIOCHEM.
                             SEQUENCE
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MEDILINE: 89061744.
MARKAWA K., SUDOH T., FURUSAWA M., MINAMINO N., KANGAWA K., OKHUBO H.,
NAKANISHI S., MATSUO H.:
                                                                                         Ξ.
                                                                                                                                                                                           NGUYEN T.T., LAZURE C., BABINSKI K., CHRETIEN M., ONG H., DE LEAN A.; "Aldosterone secretion inhibitory factor: a novel neuropeptide in
                                                                                                                                                                                                                                                                                                                                                                                           GAMMA-BRAIN NATRIURETIC PEPTIDE.
ALDOSTERONE SECRETION INHIBITORY FACTOR.
BRAIN NATRIURETIC PEPTIDE (BNP-26).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                           bovine chromaffin cells...

Brockingly 44.1591-1593(1989)...

-!- FUNCTION: INHIBITS ALDOSTERONE SECRETION...

-!- FUNCTION: VASOACTIVE ACTIVITY...

-!- TISSUE SPECIFICITY: BRAIN AND ALSO IN ATRIA, BUT AT MUCH LOWER LEVELS THAN ANP...

-!- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY...
                                                                                      NGUYEN T.T., LAZURE C., BABINSKI K., CHRETIEN M., DE LEAN A., ONG "Purification and primary structure of pro-aldosterone secretion inhibitory factor from bovine adrenal chromaffin cells."; MOL. ENDOCRINOL. 3:1823-1829(1989).
              EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
RRTIODACTYLA; RUMINANTIA; PECORA; BOYOIDEA; BOVIDAE; BOS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEWICKI J.A., SEILHAMER J.J.; "Cloning of a cDNA encoding porcine brain natriuretic peptide."; J. BIOL. CHEM. 264:6689-6692(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Isolation and identification of a high molecular weight brain natriuretic peptide in porcine cardiac atrium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
ARTIODACTYLA; SUIFORMES; SUINA; SUIDAE; SUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Cloning and sequence analysis of cDNA encoding a precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PORTER J.G., ARFSTEN A., PALISI T., SCARBOROUGH R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 160; DB 1; Le
Pred. No. 3.01e-20;
7; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                porcine brain natriuretic peptide.";
BIOCHEM. BIOPHYS. RES. COMMUN. 157:410-416(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 LRAL-RGPKMMRDSGCFGRRLDRIGSLSGLGCNVLRRY 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LRALLTAPRSLRRSSCFGGRÆDRIGAQSGLGCNSFR-Y 37
                                                                                                                                                                                                                                                                                                                                                                                                                        78 103 BRAIN NATRIURETIC
81 97
103 AA; 11249 MW; E3823460 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1988 (REL. 07, CREATED)
01-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
01-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
BRAIN NATRIURETIC PEPTIDE PRECURSOR (BNP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 AA
                                                                                                                                                                                                                                                                                                                               PIR; Ā41403; A41403.
PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 89061743.
MINAMINO N., KANGAWA K., MATSUO H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                              PFAM; PF00212; ANP; 1
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                                                                                                                                                                 69-103.
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les 23; Consei
                                                        SEQUENCE.
MEDLINE: 90114187.
                                                                                                                                                                                                                                                                                                                                                                           VASOACTIVE; BRAIN.
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                                                                                                                                                                               89136947
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                                                                                                                                                                 SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
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P07634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                           PEPTIDE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                         STRUCTURE BY NMR OF BNP-26.
MEDLINE, 91031435.
INOORA H., KIKUCHI T., ENDO S., ISHIBASHI Y., WAKIMASU M., MIZUTA E.;
"Conformation in solution of portine brain natriuretic peptide
determined by combined use of nuclear magnetic resonance and distance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRAIK D., MUNCO S., NIELSEN K., SHEHAN P., TREGEAR G., WADE J.;
"The conformation of porcine-brain natriuretic peptide by two-
dimensional NMR spectroscopy.";
EUR. J. BICCHEM. 201:183-191(1991)
-!- FUNCTION: VASOACTIVE ACTIVITY.
-!- TISSUE SPECIFICITY: BRAIN AND ALSO IN ATRIA, BUT AT MUCH LOWER
LEVELS THAN ANP.
-!- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
MEDULINE; 883,3937.
SUDOH T., MINAMINO N., KANGAWA K., MATSUO H.;
SUDOH T., MINAMINO N., KANGAWA K., MATSUO H.;
"Brain natrilymetic peptide-32: N-terminal six amino acid extended
form of brain natrilymetic peptide identified in porcine brain.";
BIOCHEM. BIOPHYS. RES. COMMUN. 155:726-732(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAMMA-BRAIN NATRIURETIC PEPTIDE.
BRAIN NATRIURETIC PEPTIDE (BNP-32)
BRAIN NATRIURETIC PEPTIDE (BNP-26)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
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14512 MW; 17699327 CRC32;
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Pred. No. 1.65e-19;
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                                                                                                                                                                                                                                   SUDOH T., KANGAWA K., MINAMINO N., MATSUO H.; "A new natriuretic peptide in porcine brain."; NATURE 332:78-81(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; S06559; S06359.
PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         geometry.";
EUR. J. BIOCHEM. 193:127-134(1990).
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P16859;
01-AUG-1990 (REL. 15, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRUCTURE BY NMR OF BNP-26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BRAIN; SIGNAL.
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'Identification of a 29-amino acid natriuretic peptide in chicken
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                                 heart.
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01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                 peptide.";
BIOCHEM. BIOPHYS. RES. COMMUN. 165:650-658(1989).
-!- FUNCTION: VASOACTIVE ACTIVITY.
-!- TISSUE SPECIFICITY: BRAIN AND ALSO IN ATRIA, BUT AT MUCH LOWER LEVELS THAN ANP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAMMA BRAIN NATRIURETIC PEPTIDE.
BRAIN NATRIURETIC PEPTIDE (BNP-34)
BRAIN NATRIURETIC PEPTIDE (BNP-29)
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AKIZUKI N., KANGAWA K., MINAMINO N., MATSUO H.;

"Cloning and sequence analysis of complementary DNA encoding precursor for chicken natituretic peptide.";
                                                                                                                                                                                                                                          SEILHAMER J.J., ARESTEN A., MILLER J.A., LUNDQUIST P., SCARBOROUGH R.M., LEWICKI J.A., PORTER J.G., "Human and canine gene homologs of porcine brain natriuretic
                                                                                                                     EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA.
CARNIVORA; FISSIPEDIA; CANIDAE; CANIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 LRRL-RSPKMMHKSGCFGRRLDRIGSLSGLGCNVLRKY 140
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DCEBCC52 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 AA
01-AUG-1990 (REL. 15, LAST SEQUENCE UPDAT
01-OCT-1996 (REL. 34, LAST ANNOTATION UPD
BRAIN NATRIURETIC PEPTIDE PRECURSOR (BNP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
PFAM; PF00212; ANP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14966 MW;
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Local Similarity 55.3%;
les 21; Conservative
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                                                                                              CANIS FAMILIARIS (DOG)
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                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                        MEDLINE; 90088474
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ANF_CHICK
P18908;
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PEPTIDE
DISULFID
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
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                                                                                                                                                          -:- A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF ATRIOPEPTINS.
                            -i- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIV SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä
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COMMUN. 155:1330-1337(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 143; DB 1; Le
Pred. No. 4.08e-16;
8; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 AA; 15714 MW; E0A8F52F CRC32;
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PIR; S14320; S14320.
PIR; A31509; A31509.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 55.6%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00212; ANP; 1. VASOACTIVE; SIGNAL.
BIOCHEM. BIOPHYS.
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Wed Jun 16 12:50:24 1999; MasPar time 6.96 Seconds 290.262 Million cell updates/sec Tabular output not generated. Run on:

1 LRALLTAPRSLRRSSCFGGRMDRIGAQSGLGCNSFRY 37 >VANDER-027-213.PEP (1-37) from vander027777.pep 279 Title: Description:. Perfect Score: Sequence:

179066 seqs, 54579741 residues PAM 150 Gap 11 Scoring table: Searched:

Minimum Match 0% Listing first 45 summaries. sptremb19 Post-processing: Database:

1:sp_archea 2:sp_bacteria 3:sp_fung1 4:sp_human 5:sp_invertebrate 6:sp_mamma1 7:sp_mhc 8:sp_organelle 9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus Mean 32.418; Variance 46.907; scale 0.691 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Pred. No	1.69e-50	1.69e-50	1.24e-48	5.58e-18	1.79e-07	2.24e-05	3.52e-03	3.15e-02	7.40e-0	1.13e-0]	3.93e-0	3.93e-0	8.88e-0	8.88e-0	1.33e+00	1.33e+00	1.33e+0(1.33e+00	1.33e+00	1.97e+00
Description	ATRIAL NATRIURETIC FAC	ATRIAL NATRIURETIC PEP	CARDIODILATIN, ATRIAL	BRAIN NATRIURETIC PEPT	BRAIN NATRIURETIC PEPT	NATRIURETIC PEPTIDE.	F1104.13 PROTEIN.	HYPOTHETICAL 21.2 KD P	GLUCOSAMINE FRUCTOSE -	F31C3.3 PROTEIN.	NEUREGULIN.	CHEMOTAXIS PROTEIN CHE	FERREDOXIN REDUCTASE.	POLYKETIDE SYNTHASE.	CONSERVED PROTEIN.	UNKNOWN (FRAGMENT).	F46F3.2.	C07E3.3 PROTEIN.	POLYPROTEIN 1A.	MC088R.
ΩI	913766	046540	029130	046541	055086	P79799	082599	029736	026948	062191	035947	055527	052437	054155	026659	083025	P90876	917786	083017	098255
8	4	9	9	9	1	13	10	٦	-	S	11	7	~	~	٦	14	S	2	14	14
Match Length DB	151	152	155	129	121	139	298	187	334	2025	461	1095	410	2297	232	419	511	1186	2206	143
Match	100.0	100.0	97.5	54.5	38.0	34.4	30.5	28.7	28.0	27.6	26.5	26.5	25.8	25.8	25.4	25.4	25.4	25.4	25.4	25.1
Score	279	279	272	152	106	96	82	80	78	77	7.4	74	72	72	71	71	71	71	71	70
NO.		7	m	4	S	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20

CREATED) LAST SEQUENCE UPDATE) LAST ANNOTATION UPDATE)

ULT 2
046540 PRELIMINARY;
046540;
046540;
046540;
01-JUN-1998 (TREMBLREL. 06, C
01-JUN-1998 (TREMBLREL. 06, L
01-AUG-1998 (TREMBLREL. 07, L
ATRIAL NATRIURETIC PEPTIDE.

RESULT 1D 04 AC 04 DT 01 DT 01 DT 01

152 AA.

· PRT;

1.97e+00	1.97e+00	1.97e+00	1.97e+00	1.97e+00	1.97e+00	1.97e+00	2.93e+00	2.93e+00	2.93e+00	2.93e+00	2.93e+00	2.93e+00	2.93e+00	4.32e+00	4.32e+00	4.32e+00	4.32e+00	4.32e+00	4.32e+00	4.32e+00	4.32e+00	6.35e+00	6.35e+00	6.35e+00
IDURONATE-2-SULFATASE.	COSMID FORF8.	IDURONATE-2-SULPHATASE	COSMID FORF8.	O-ACETYLSERINE-(THIOL)	C16A3.2 PROTEIN.	ORF1, ORF2, AND ORF3.	PHYTOCHROME (FRAGMENT)	RETINOIC ACID RECEPTOR	KIAA0396 (FRAGMENT).	ENDO-GLUCANASE.	2A PROTEIN.	CMV-SD 2A.	SIMILAR TO THE C. ELEG	HYPOTHETICAL.	TRAI.	HYPOTHETICAL 28.0 KD P	HYPOTHETICAL 36.0 KD P	HYPOTHETICAL 46.0 KD P	PHOSPHOMANNOMUTASE.	ALPHA ESTERASE.	ETS HOMOLOGUE.	PVI PROTEIN (FRAGMENT)	UNKNOWN PRODUCT.	TAR DNA-BINDING PROTEI
060597	019208	014604	019209	033137	Q18038	069340	009236	P79878	043146	052747	083261	066144	001526	083011	066168	054085	065569	006634	051847	024197	026645	064828	052960	013148
4	Ŋ	4	S	œ	S	14	10	13	4	~	14	14	Ŋ	14	~	~	14	~	~	ഗ	ഗ	14	~	4
179	281	343	352	390	1810	1958	192	442	601	680	857	828	1121	64	211	251	339	433	470	541	559	45	307	414
25.1	25.1	25.1	25.1	25.1	25.1	25.1	24.7	24.7	24.7	24.7	24.7	24.7	24.7	24.4	24.4	24,4	24.4	24.4	24.4	24.4	24.4	24.0	24.0	24.0
70	70	70	70	70	70	70	69	69	69	69	69	69	69	99	. 68	89	89	89	89	89	89	67	29	67
21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

NAKY; PRT; 151 AA.	01, CREAT	REL. 01, LAST SEQUENCE UPDATE)	REL. 09, LAST ANNOTATION UPDATE)	FACTOR PRECURSOR.	0,	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;	AE; ·HOMO.				SEIDMAN C.E., BLOCH K.D., ZISFEIN J., SMIT J., HABER E., HOMCY C.,	DUBY A.D., CHOI E., GRAHAM R.M., SEIDMAN J.G.;	"Molecular studies of the atrial natriuretic factor gene.";	4(1985).	38;	38; JOINED.	PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.			25		ATF	146 BY SIMILARITY.	16381 MW; E8827DA3 CRC32;	100.0%: Score 279: DB 4: Length 151:			115 LRALLTAPRSLRRSSCFGGRMDRIGAOSGLGCNSFRY 151	
PRELIMINARY;	(TREMBLREL. 01,	(TREMBLREL.	(TREMBLREL.	ATRIAL NATRIURETIC FACTOR PRECURSOR.	IS (HUMAN).	METAZOA; CHORDATA;	CATARRHINI; HOMINIDAE; HOMO.		OM N.A.	85205210.	I., BLOCH K.D., ZISI	CHOI E., GRAHAM R.1	studies of the atr.	HYPERTENSION 7:31-34(1985).	EMBL; M54947; G178638;	EMBL; M54951; G178638; JOINED.	300263; NATRIURETIC	PFAM; PF00212; ANP; 1.	SIGNAL.	25	55	151	_	151 AA; 16381 MW;				TAPRSLRRSSCFGGRMDRIC	
RESULT 1. ID 013766	Q13/66; 01-NOV-1996	01-NOV-1996	01-JAN-1995	ATRIAL NATE	HOMO SAPIENS (HUMAN)	EUKARYOTA ;	CATARRHINI;	. (1)		MEDLINE; 85	SEIDMAN C.E	DUBY A.D.,	"Molecular	HYPERTENSIC	EMBL; M5494	EMBL; M5495	PROSITE; PS	PFAM; PF002	VASOACTIVE; SIGNAL.	SIGNAL	PEPTIDE	PEPTIDE	DISULFID	SEQUENCE	Onerv Match	lest Local Sin	Matches 37;	115 LRALL	-
RES	된	DŢ	D	DE	SO	႘	8	RN	RP	RX	RA	RA	RŢ	RL	DR	DR	N.	DR	ΚW	FT	FI	FT	F	SO	C	ıЩ	24	đ	

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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
IISSUE=VENOM GLAND;
MEDLINE; 98092299.
HO P.L., SOARES M.B., MAACK T., GIMENEZ I., PUORTO G., FURTADO M.F.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAMURA N., OGAWA Y., YASODA A., NAKAO K.;
"Two cardiac natriuretic peptide genes (atrial natriuretic peptide and brain natriuretic peptide) are organized in tandem in the mouse and human genomes.";
                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MICRURUS CORALLINUS.
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; LEPIDOSAURIA; SQUAMATA;
SCLEROGLOSSA; SERPENTES; COLUBROIDEA; ELAPIDAE; ELAPINAE; MICRURUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OGAWA Y., ITOH H., TAMURA N., SUGA S., YOSHIMASA T., UEHIRA M., MATSUDA S., SHIONO S., NISHIMOTO H., NAKAO K.;
"Molecular cloning of the complementary DNA and gene that encode mouse brain natriuretic peptide and generation of transgenic mice that overexpress the brain natriuretic peptide gene.";
J. CLIN. INVEST. 93:1911-1921(1994).
                                                                                                     .;
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Pred. No. 1.79e-07;
6; Mismatches 3; Indels
                                       Length 129
                                Score 152; DB 6; Length 125
Pred. No. 5.58e-18;
8; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                93 LQAL-RGPKMMRDSGCFGRRLDRIGSLSGLGCNVLRRY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D82049; D10250by; -. PROSITE; PS00263; NATRIURETIC_PEPTIDE: 1.
                                                                                                                                                                                              139 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L. CELL. CARDIOL. 28:1811-1815(1996)
D82049; D1025069; -.
                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE-VENOM GLAND;
HO P.L., SOARES M.B., YAMANE T., RAW I.;
J. TOXICOL. TOXIN. REV. 14:327-337(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CREATED)
                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 SSCFGHKIDRIGSVSRLGCNALK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |||||| ::||||: | ||||:::
14 SSCFGGRMDRIGAQSGLGCNSFR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 60.9%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1998 (TREMBLREL. 06, 01-NOV-1998 (TREMBLREL. 08, BRAIN NATRIURETIC PEPTIDE.
                                Query Match
Best Local Similarity 57.9%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      (TREMBLREL: 06,
                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1997 (TREMBLREL. 01-NOV-1998 (TREMBLREL. NATRIURETIC PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1997 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUS MUSCULUS (MOUSE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 94237953.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 97031884.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-129/SV;
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                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1998 (
01-JUN-1998 (
01-NOV-1998 (
                                                                                                                                                                                                                                                                                                                    LT 5
055086
055086;
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P79799
P79799;
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                                                                                                                                                                                                                                                                                                                       SOLATOR SOLATO
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ANP.
OVIS ARIES (SHEEP),
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
ARIODACTYLA; RUMINANTIA; PECORA; BOVOIDEA; BOVIDAE; CAPRINAE; OVIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OVIS ARIES (SHEEP).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
ARTIODACTYLA; RUMINANTIA; PECORA; BOVOIDEA; BOVIDAE; CAPRINAE; OVIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                SEQUENCE FROM N.A.
AITKEN G.D., RAILIS A.M., GEORGE P.M., ESPINER E.A., CAMERON V.A.,
SUBMITTED (DEC-1908) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL, AF031465; G2708650; -.
PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
SEQUENCE 152 AA; 16368 MW; D5360BCC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AITKEN G.D., RAIZIS A.M., GEORGE P.M., ESPINER E.A., CAMERON V.A.; SUBMITTED (DEC-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL: AF037466; G7108652;
PROSITE: PS00203; NATURETIC_PEPTIDE; 1.
SEQUENCE 129 AA; 14118 MW; 85DE4222 CRC32;
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SCANDENTIA; TUPAIIDAE; TUPAIA.
                                                                                                                                                                                                                                                                                                                                                                               Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCHNEIDEMANN S., MAEGERT H.J., FORSSMANN W.G.;
SUBMITTED (MAR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBMITTED (MAR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; Z70294; E233859; -.
PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
CARDIODILATIN, ATRIAL NATRIURETIC PEPTIDE.
TUPAIA BELANGERI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               046541 PRELIMINARY; PRT; 129 AA.
046541 046541
01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
BRAIN NATRIURETIC PEPTIDE.
                                                                                                                                                                                                                                                                                                                                              Score 279; DB 6; Ler
Pred. No. 1.69e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 272; DB 6; L6
Pred. No. 1.24e-48;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 LRALLTAPRSLRRSSCFGGRMDRIGAQSGLGCNSFRY. 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM: PF00112; ANP; 1.
SEQUENCE 155 AA; 16860 MW; 77E8CA8B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 LRAMLAAPRSLRRSSCFGGRMDRIGAQSGLGCNSFRY 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LRALLTAPRSLRRSSCFGGRMDRIGAQSGLGCNSFRY 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%;
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 94.6%;
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LISSUE-HEART
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 3
ID Q29130
AC Q29130;
      SORRERES
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KLENK H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E.,
KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,
RICHARDSON D.L., KELLAYAGE A.R., GRAHAM D.E., KYRPIDES N.C.,
FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,
RIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,
PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODER A., ZHOU
OVERBEEK R., GOCARNE J.D., WELDMAN J.F., MCDONALD L., UTTERBACK T.,
SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,
MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 28.0%;
Best Local Similarity 43.3%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 44.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   062191 PRELIMINARY;
062191 OC5191,
01-303-1998 (TREMBLREL, 0
01-306-1998 (TREMBLREL, 0
01-3AN-1999 (TREMBLREL, 0
                                                                                                                                                                                                                                                                                                                                                                              11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                        HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-DELTA H;
MEDLINE; 98037514
                                                                                                                                                                                      VENTER J.C.
                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LT 9
026948
026948;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
              "Cloning of an unusual natriuretic peptide from the South American coral snake Micrurus corallinus.";
EUR. J. BIOCHEM. 250:144-149(1997).
EMBL; U77596; G1684874;
PROSITE: PS002025; NATRIURETIC_PEPTIDE; 1.
SPRAM: PF00212; ANP; 1.
SEQUENCE. 139 AA: 14881 MW; 05421ABB CRC32;
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ARCHAEA; EURYARCHAEOTA; ARCHAEOGLOBALES; ARCHAEOGLOBACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STAIN-CV. COLUMBING T., LANGSTON Y., TREVASKIS E.;
ABU-THREIDEH J., STONEKING T., LANGSTON Y., TREVASKIS E.;
The sequence of A. thaliana F1104.";
SUBMITTED (OCT-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 298;
                                                                                                                                                    34.4%; Score 96; DB 13; Length 139; 59.1%; Pred. No. 2.24e-05;
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                                                                                                                                                                                      6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The A. thaliana Genome Sequencing Project.";
SUBMITTED (OCT-1998) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                            08, CREATED)
08, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF096370; G3695384; -.
SEQUENCE 298 AA; 33450 MW; 61E11354 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187 AA.
                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                              298 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-VC-16 / DSM 4304 / ATCC 49558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                        85 GCFGQRIDRICNVSGMGCNHVR 106
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01-AUG-1998 (TREMBLREL. 07, L
HYPOTHETICAL 21.2 KD PROTEIN.
                                                                                                                                                    Query Match
Best Local Similarity 59.1%;
Matches 13; Conservative
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01-NOV-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
F1104.13 PROTEIN.
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WATERSTON R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
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082599
082599;
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                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALDREDGE T., BASHIRZADER R., BLAKELY D., COOK R., GILBERT K.,
HARRISON D., HOANG L., KEAGLE P., LUMM W., POTHIER B., QIU D.,
SPADAPORA R., VICARE R., WANG Y., WIERZBOWSKI J., GIBSON R.,
JIWANI N., CARUSO A., BUSH D., SAFER H., PATWELL D., PRABHAKAR S.,
MCDOUGALL S., SHIMER G., GOYAL A., PIETROVSKI S., CHURCH G.M.,
DANIELS C.J., MAO J.-I., RICE P., NOLLING J., REEVE J.N.;
"Complete genome sequence of Methanobacterium thermoautotrophicum
deltah: functional analysis and comparative genomics.";
J. BACTERIOL, 179:7135-7155(1997).

EMBL: AEGO00662: G.2621952;
TRANSFERASE: AMINOTRANSFERASE
SEQUENCE 334 AA; 37853 MM; B5B5BA4C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METHANOBACTERIUM THERMOAUTOTROPHICUM.
ARCHARA; EURYARCHAEOTA; METHANOBACTERIALES; METHANOBACTERIACEAE;
METHANOBACTERIUM.
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                                                                                                                                                                                                Length 187;
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                                                                                                                                                                                                                                             Indels
01-Jan-1998 (TREMBLREL. 05, CREATED)
01-Jan-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-Jang-1998 (TREMBLEEL. 07, LAST ANNOTATION UPDATE)
GLUCOSAMINE-FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE.
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                Score 80; DB 1; Len
Pred. No. 3.15e-02;
8; Mismatches 6;
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Pred. No. 7.40e-02;
                                                                                                                                           187 AA; 21243 MW; D7BE7C22 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    334 AA
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                                                                                                                                                                                                                                                                                           21 ALLCPPHPLMGGSRFDVRLERIAAE 45
                                                                                                                                                                                                                                                                                                                      3 ALLTAPRSLRRSSCFGGRMDRIGAQ 27
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Gaps
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MEDLINE: 97061201.

KANEKO I., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
MIYAJIWA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S.
SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. PCG6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA RES. 3:109-136(1996).
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                                                                                                                                                                                       STRAIN-FCC6803;
MEDLINE; 96127529.
KANEKO I., TABATA A., SATO S., KOTANI H., SAZUKA T., MIYAJIMA N., SUGIURA M., TABATA S.;
SUGIURA M., TABATA S.;
"Sequence analysis of the genome of the unicellular cyanobacterium Sequence analysis of the genome of the genome features in the 1Mb region from map positions 64% to 92% of the genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-KKS102;
MEDLINE; 94179104.
KIKUCHI Y., NAGATA Y., HINATA M., KIMBARA K., FUKUDA M., YANO K.,
TAKAGI M.;
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Pred. No. 3.93e-01;
5; Mismatches 8; Indels
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                                SYNECHOCYSTIS SP. (STRAIN PCC 6803).
BACTERIA; CYANOBACTERIA; CHROOCOCCALES; SYNECHOCYSTIS.
                                                                                                                     TABATA S.;
SUBMITTED (AUG-1995) TO EMBL/GENBANK/DDBJ DATA BANKS
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LAST ANNOTATION UPDATE)
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PFAM; PF00512; signal; 1.
SEQUENCE 1095 AA; 120557 MW; 6697EB16 CRC32;
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Best Local Similarity 40.9%;
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CHEMOTAXIS PROTEIN CHEA
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                                                                                   SEQUENCE FROM N.A. STRAIN-PCC6803;
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Q52437
Q52437;
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MESOCRICETUS AURATUS (GOLDEN HAMSTER).
EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCIUROGNATHI; MURIDAE; CRICETINAE; MESOCRICETUS.
                                                                                                                                                               MEDLINE; 94150718.
MEDLINE; 94150718.
MEDLINE; 94150718.
MILSON R., AINDERSON K., BAYNES C., BERKS M.,
WILSON R., AINDERSON K., COPER J., COOPER J., COLESON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAM J., KIRSTEN J., LATREILLE P.,
LIGHTWING J., LLOYD C., MOUNTRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
SMALDON N., SMITH A., SONNHAAMER E., STADEN R., GUISTON J.,
HIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN R., WOHLDMAN P.,
THERRY-MIEG J., THOMAS K., VAUDIN M., WOHLDMAN P.,
TO MARK MALLEND A., WILKINSON-SPROAT J., WOHLDMAN P.,
TO M. MELNSTOK L., WILKINSON-SPROAT J., WOHLDMAN P.,
TO M. CONTIGUOUS NUCLEOUTIGE SEQUENCE FROM Chromosome III of C.
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                                                EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
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Pred. No. 3.93e-01;
9; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 77; DB 5; Length 2025;
Pred. No. 1.13e-01;
7; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COTTAGE A.;
SUBMITTED (MAR-1997) TO EMBL/GENBANK/DDBJ DATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                             NATÚRE 368:32-38(1994).
EMBL; 292784; E1346409; -.
SEQUENCE 2025 AA; 234375 MW; CF2EB634 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           461 AA; 50890 MW; E937DA34 CRC32;
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01-JAN-1998 (TREMBLREL. 05,
01-NOV-1998 (TREMBLREL. 08,
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Local Similarity 37.5%;
Hes 12; Conservative
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Best Local Similarity 42.9%;
Matches 9; Conservative
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05527 05527;
01-807-1996 (TREMBLREL. 0
01-NOV-1996 (TREMBLREL. 0
01-JAN-1999 (TREMBLREL. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
              F31C3.3.
CAENORHABDITIS ELEGANS
                                                                                                   SEQUENCE FROM N.A.
F31C3.3 PROTEIN.
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035947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REDENBACH M., KIESER H.M., DENAPAITE D., EICHNER A., CULLUM J., KINASHI H., HOPWOOD D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicola A3(2) chromosome.";
MOL. MICROBIOL. 21:77-96[1996).
EMBL: AL021409; E1245723; -.
PROSITE: PS00606; B_KETOACYL_SYNTHASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMITH D.R., DOUCETTE-STAMM L.A., DELOUGHERY C., LEE H.-M., DUBOIS , ALDREDGE T., BASHIRZADEH R., BLAKELY D., COOK R., GILBERT K., STARRISON D., HOANG L., KERGLE P., LUMM W., POTHIER B., QIU D., SPADAFONA R., VICARE R., WANG Y., WIERZBOWSKI S., GIBSON R., JIMANI N., CARUSO A., BUSH D., SAFER H., PATWELL D., PRABHAKAR S., MCDOUGALL S., SHIMER G., GOYAL A., PIETROVSKI S., CHURCH G.M., DANIELS C.J., MAO J.-I., RICE P., NOLLING J., REEVE J.N.;
                                                                                                                                                                                                                                                                                                               STREFTOMYCES COELICOLOR.
BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
ACTINOMYCETALES; STREPTOMYCINEAE; STREPTOMYCETACEAE; STREPTOMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete genome sequence of Methanobacterium thermoautotrophicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                METHANOBACTERIUM THERMOAUTOTROPHICUM.
ARCHAEA; EURYARCHAEOTA; METHANOBACTERIALES; METHANOBACTERIACEAE;
METHANOBACTERIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 72; DB 2; Length 2297;
Pred. No. 8.88e-01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           deltaH: functional analysis and comparative genomics."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-A3(2);
PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
SUBMITTED (JAN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=A3(2);
OLIVER K., HARRIS D.;
SUBMITTED (JAN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                           01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
POLYKETIDE SYNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1998 (TREMBLREL. 05, CREATED)
01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2297 AA; 241989 MW; 24BE710A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              232 AA
                                                                                                                                2297 AA
1058 LIAPRSTAGRAVMIGALERAGVQPG 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                PRT;
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Best Local Similarity 44.0%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-DELTA H;
MEDLINE; 98037514.
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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MEDLINE; 97000351
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026659
026659;
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Gaps
                                                                                                                                        5;
                                                                                        Query Match 25.4%; Score 71; DB 1; Length 232; Best Local Similarity 37.9%; Pred. No. 1.33e+00; Matches 11; Conservative 5; Mismatches 11; Indels
J. BACTERIOL. 179:7135-7155(1997).
EMBL; AE0000838; G2621635; -.
SEQUENCE 232 AA; 26259 MW; B9545E8B CRC32;
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99 LVLPHCLRNPEC-EARLERTGLICT-GCN 125

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Search completed: Wed Jun 16 12:51:22 1999 Job time : 58 secs.